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                256                              422
   SGK      TTSTFCGTPEYLAPE........FLGFSYAPP


                308                              473
   PKBα     TMKTFCGTPEYLAPE........FPQFSYSAS


                229                              389
   p70 S6K  VTHTFCGTIEYMAPE........FLGFTYVAP


                507                              664
   PKCδ     RASTFCGTPDYIAPE........FAGFSFVNP
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(57) Abstract

A method of activating serum and glucocorticoid–induced protein kinase (SGK) is provided wherein the SGK is phosphorylated. The SGK may be phosphorylated by PDK1 and/or a preparation containing PDK2 activity. A method of identifying a compound that modulates the activity of SGK is provided, wherein the activity of SGK is measured by measuring the phosphorylation by SGK of a polypeptide comprising an amino acid sequence corresponding to the consensus sequence (Arg/Lys; preferably Arg)-X-(X/Arg)-X-X-(Ser/Thr)-Z wherein X indicates any amino acid, X/Arg indicates any amino acid, with a preference for arginine, and Z indicates that the amino acid residue is preferably a hydrophobic residue. The SGK may be activated by phosphorylation.

METHODS

The present invention relates to screening methods for new drugs or lead compounds.

5   Protein kinase B (PKB) (also called c-Akt or RAC kinase) is believed to play a key role in mediating many of the metabolic actions of insulin, as well as the anti-apoptotic effects of survival factors such as insulin-like growth factor-1 (IGF-1) (reviewed in [1,2]). PKB is activated within a few minutes in response to insulin or survival factors *via* a

10   phosphatidylinositol (PtdIns) 3-kinase dependent mechanism [3-5]. Activation results from the phosphorylation of Thr308 and Ser473, and the phosphorylation of both residues is prevented by inhibitors of PtdIns 3-kinase [6]. 3-phosphoinositide-dependent protein kinase-1 (PDK1) phosphorylates Thr308, which is located in the "activation loop" between

15   subdomains VII and VIII of the catalytic domain, *in vitro* [7-9], and can be converted to a form that phosphorylates Ser473, which lies close to the C-terminus, as well as Thr308 upon interaction with a peptide corresponding to the C-terminal sequence of protein kinase C-related kinase-2 (PRK2) (Balendran *et al* (1999) *Curr. Biol.* 9, 393-404).

20   However, whether Ser473 is phosphorylated *in vivo* by PDK1 remains to be established.

       The activation of PKB by PDK1 *in vitro* only takes place in the presence of lipid vesicles containing PtdIns(3,4,5)P_3, the product of the PtdIns 3-

25   kinase reaction, and results from the interaction of this "second messenger" with the pleckstrin homology (PH) domains of both PKB and PDK1 [9, 10].

2

PtdIns(3,4,5)P$_3$ is associated with the inner leaflet of the plasma membrane. The insulin or IGF-1 induced increase in PtdIns(3,4,5)P$_3$ is therefore accompanied by the recruitment of PKB from the cytosol to the plasma membrane where it becomes activated [12, 13]. Membrane

5   recruitment appears to facilitate activation by PDK1 and PDK2 [12]. PDK1 binds to PtdIns(3,4,5)P$_3$ much more avidly than does PKB [10], and an interaction of PDK1 with the low levels of PtdIns(3,4,5)P$_3$ present under basal conditions may explain, at least in part, its constitutive association with the plasma membrane. Translocation of PDK1 from the

10   cytosol to the plasma membrane in response to IGF-1 or PDGF may occur [14].

The amino acid sequence immediately C-terminal to Thr308 of PKB is similar to that found in other protein kinases that play important roles in

15   signal transduction, such as p70 S6 kinase and protein kinase C (Fig 1). PDK1 activates p70 S6 kinase [15, 16], PKCδ and PKCζ [17, Chou *et al* (1998) *Curr Biol* 8, 1069-1077] *in vitro*, and in cotransfection experiments, by phosphorylating the residue equivalent to Thr308 of PKB. The activation of p70 S6 kinase by PDK1 *in vitro* is not affected by

20   PtdIns(3,4,5)P$_3$.

Like PKB, p70 S6 kinase and PKC contain the proposed consensus sequence for phosphorylation by the protein kinase activity termed PDK2 (Phe-Xaa-Xaa-(Phe/Tyr)-(Ser/Thr)-(Phe/Tyr)), which is always located

25   160-165 residues C-terminal to the PDK1 phosphorylation site (Fig 1). These observations suggest that PDK1 and the protein kinase activity termed PDK2 may participate together in the activation of a number of protein kinases. A PDK2 activity has been characterised (Balendran *et al* (1999) *Curr. Biol.* 9, 393-404; UK patent application No 9906245.7 filed

19 March 1999 and Alessi *et al* US patent application filed 2 December 1999).

Serum and glucocorticoid-induced protein kinase (SGK) was originally
5   identified in a differential screen aimed at finding glucocorticoid-inducible
transcripts [18]. The levels of SGK mRNA and protein are both elevated
5-10 fold, with a half time of 30 min in Rat2 fibroblasts, following cell
stimulation with serum or glucocorticoids [19]. SGK is also induced in
response to other stimuli, such as follicle-stimulating hormone [20],
10   increased extracellular osmolarity [21], injury of the brain [22, 23] and by
transfection of mammary epithelial cells with p53 [24]. However, the
glucocorticoid-stimulated induction of SGK is suppressed by wild type p53
in Rat2 fibroblasts, but not by mutant p53 [25].

15   The structure of SGK is similar to PKB, but it lacks a PH domain. The
catalytic domain of SGK is 54% identical to PKB, 50% identical to p70 S6
kinase and 48% identical to PKC.

We demonstrate here that SGK is activated by IGF-1 or an oxidative stress
20   in 293 cells via a PtdIns 3-kinase-dependent pathway. Activation appears
to result from phosphorylation. Further, SGK possesses a threonine
residue at the position equivalent to Thr308 of PKB and a serine residue
equivalent to Ser473, and the sequences surrounding these residues are
consistent with an ability to be phosphorylated by PDK1 and a PDK2
25   activity (Fig 1). Activation appears to result from phosphorylation of the
residues equivalent to Thr308 and Ser473, and the residue equivalent to
Thr308 is phosphorylated and SGK activated by PDK1 *in vitro*. SGK
preferentially phosphorylates serine and threonine residues that lie in an

4

Arg-Xaa-Arg-Xaa-Xaa-(Ser/Thr)- motif, and inactivates glycogen synthase kinase-3 (GSK3) at similar rates to PKB *in vitro*.

We further identify novel isoforms of SGK, termed SGK2 and SGK3, that
5   are activated in a similar manner to the previously identified SGK [18] (herein termed SGK1). The catalytic domains of SGK2 and SGK3 share 80% amino acid sequence identity with each other and with SGK1.

10 A first aspect of the invention is a method of activating serum and glucocorticoid-induced protein kinase (SGK) wherein the SGK is phosphorylated. The SGK that is activated by the method may be partially or fully deactivated/dephosphorylated SGK.

15 A further aspect of the invention is a method of reducing the activity of SGK wherein the SGK is dephosphorylated. The SGK the activity of which is reduced may be partially or fully activated/phosphorylated SGK.

By "activating" is meant that the enzymatic activity of SGK is increased.
20 By "reducing the activity" is meant that the enzymatic activity of SGK is reduced. The enzymatic activity that may be increased or reduced is protein kinase activity, preferably Serine/Threonine protein kinase activity ie the phosphorylation of a protein/polypeptide on one or more serine or threonine residues. The enzymatic activity may be increased or reduced
25 by an alteration in the V_{max} or the K_m (or both) of the SGK for a particular substrate. For example, activity may be increased by an increased V_{max} or decreased K_m. It will be appreciated that it may not be necessary to determine the value of either V_{max} or K_m in order to determine whether the

5

SGK has been activated or deactivated. It will be appreciated that dephosphorylated (deactivated) SGK may retain some enzymatic activity.

Activity may be measured as the amount of a substrate phosphorylated in a

5   given time; a change of activity may therefore be detected as a change in the amount of substrate (for example, at a single concentration) that is phosphorylated in a given time, as described in Example 1. The substrate may be a polypeptide comprising the consensus sequence Arg-X-(X/Arg)-X-X-(Ser/Thr)-Z where X indicates any amino acid, X/Arg indicates any

10   amino acid, with a preference for arginine, and Z indicates that the amino acid residue is preferably a hydrophobic residue. An example of such a polypeptide is the peptide Crosstide (GRPRTSSFAEG). The underlined residue may be phosphorylated by the said protein kinase. Other examples of polypeptides that may be substrates of SGK are shown in

15   Table 1 and Table 2. Glycogen synthase kinase-3 (GSK3) may be a substrate of SGK, as discussed in Example 1.

It will be appreciated that if the SGK is already phosphorylated, further phosphorylation may not be possible and/or may not lead to further

20   activation. Further, if the SGK is already partially dephosphorylated, then further dephosphorylation may not be possible and/or may not lead to further deactivation.

It will further be appreciated that SGK isolated from cells (either as an

25   endogenous or recombinant polypeptide) may be heterogeneous with regard to its phosphorylation/activation state. For example, fully activated/phosphorylated, fully deactivated/dephosphorylated and/or partially activated/phosphorylated molecules of SGK may be present in a single cell or group/culture of cells.

6

It is preferred that the activity is increased or decreased, as appropriate, by at least 2, preferably 5, 10, 15, 20, 25, 30 or 50-fold.

5   By serum and glucocorticoid-induced protein kinase (SGK) is included a polypeptide, preferably a protein kinase, encoded by I.M.A.G.E Consortium clone ID 42669 (which comprises a full-length cDNA from a human infant brain library identified as encoding human serum and glucocorticoid-induced protein kinase). The term serum and

10   glucocorticoid-induced protein kinase is well known to those skilled in the art (see, for example, references 18 to 25). The amino acid sequence of human serum and glucocorticoid-induced protein kinase (herein termed SGK1) may have the Genbank accession reference Y10032. The amino acid sequence of rat serum and glucocorticoid-induced protein kinase may

15   have the Genbank accession reference L01624. Nematode (*Caenorhabditis elegans*) serum and glucocorticoid-induced protein kinase may be encoded by a portion of the 26 kb fragment from chromosome 3 genomic DNA with the accession number 281140.

20   By serum and glucocorticoid-induced protein kinase (SGK) is further included a polypeptide (termed SGK2) having the amino acid sequence

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRK
SDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLY
FVLDYVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENI
25   LLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCL
GAVLYEMLHGLPPFYSQDVSQMYENILHQPLQIPGGRTVAACDLLQSLLHKDQRQ
RLGSKADFLEIKNHVFFSPINWDDLYHKRLTPPFNPNVTGPADLKHFDPEFTQEA
VSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILDC

30   or

MQGLLTSGRKPSGGGRCTGRGGWRGQWCLKPWMGGADPPTPTLSCLLLPVPPELP
DHCYRMNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVL
LAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQT
35   PEKLYFVLDYVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDL

7

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KPENILLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAV
DWWCLGAVLYEMLHGLPPFYSQDVSQMYENILHQPLQIPGGRTVAACDLLQSLLH
KDQRQRLGSKADFLEIKNHVFFSPINWDDLYHKRLTPPFNPNVTGPADLKHFDPE
FTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILDC
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5

or

```
MASSPVGVPSPQPSRANGNINLGPSANPNARPTDFDFLKVIGKGNYGKVLLAKRK
SDGAFYAVKVLQKKSILKNKEQNHIMAERNVLLKNVRHPFLVGLRYSFQTPEKLY
FVLDYVNGGELFFHLQRERRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENI
LLDCQGHVVLTDFGLCKECVEPEETTSTFCGTPEYLAPEVLRKEPYDRAVDWWCL
GAVLYEMLHGLPPFFNTDVAQMYENILHQPLQIPGGRTVAACDLLQGLLHKDQRQ
RLGSKEDFLDIKNHMFFSPINWDDLYHKRLTPPFNPNVEGPADLKHFDPEFTQEA
VSKSIGCTPDTVASSSGASSAFLGFSYAQDDDDILDS
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10

15

The first sequence is that of human SGK2α, the second that of human
SGK2β and the second sequence is that of mouse SGK2. SGK2β has an
N-terminal 60 amino acids that are not present in SGKα.

20   By serum and glucocorticoid-induced protein kinase (SGK) is still further
included a polypeptide (termed SGK3) having the amino acid sequence

```
MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSP
KHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVL
LAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQT
TEKLYFVLDFVNGGELFFHLQRERSFPEHRARFYAAEIASALGYLHSIKIVYRDL
KPENILLDSVGHVVLTDFGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTV
DWWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELLE
KDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTA
FTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSYAPPSEDLFL
```

25

30

An alignment of the sequences of SGK1, 2, 3 and mouse SGK2 is shown
in Figure 13.

A further aspect of the invention provides a substantially pure polypeptide
35   comprising the amino acid sequence

```
MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRK
SDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLY
FVLDYVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENI
LLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCL
GAVLYEMLHGLPPFYSQDVSQMYENILHQPLQIPGGRTVAACDLLQSLLHKDQRQ
RLGSKADFLEIKNHVFFSPINWDDLYHKRLTPPFNPNVTGPADLKHFDPEFTQEA
VSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILDC
```

40

or

```
MQGLLTSGRKPSGGGRCTGRGGWRGQWCLKPWMGGADPPTPTLSCLLLPVPPELP
DHCYRMNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVL
LAKRKSDGAFYAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQT
PEKLYFVLDYVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDL
KPENILLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAV
DWWCLGAVLYEMLHGLPPFYSQDVSQMYENILHQPLQIPGGRTVAACDLLQSLLH
KDQRQRLGSKADFLEIKNHVFFSPINWDDLYHKRLTPPFNPNVTGPADLKHFDPE
FTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILDC
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or

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MASSPVGVPSPQPSRANGNINLGPSANPNARPTDFDFLKVIGKGNYGKVLLAKRK
SDGAFYAVKVLQKKSILKNKEQNHIMAERNVLLKNVRHPFLVGLRYSFQTPEKLY
FVLDYVNGGELFFHLQRERRFLEPRARFYTAEVASAIGYLHSLNIIYRDLKPENI
LLDCQGHVVLTDFGLCKECVEPEETTSTFCGTPEYLAPEVLRKEPYDRAVDWWCL
GAVLYEMLHGLPPFFNTDVAQMYENILHQPLQIPGGRTVAACDLLQGLLHKDQRQ
RLGSKEDFLDIKNHMFFSPINWDDLYHKRLTPPFNPNVEGPADLKHFDPEFTQEA
VSKSIGCTPDTVASSSGASSAFLGFSYAQDDDDILDS
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or

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MALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSP
KHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVL
LAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQT
TEKLYFVLDFVNGGELFFHLQRERSFPEHRARFYAAEIASALGYLHSIKIVYRDL
KPENILLDSVGHVVLTDFGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTV
DWWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELLE
KDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTA
FTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSYAPPSEDLFL
```

or a variant, fragment, fusion or derivative thereof, or a fusion of a said
variant or fragment or derivative. The said variant, fragment, fusion or
derivative thereof is preferably a protein kinase, more preferably a protein
kinase that is capable of phosphorylating a polypeptide comprising the
consensus Arg-X-(X/Arg)-X-X-(Ser/Thr)-Z, as discussed further below,
and is not SGK1, PKBα, PKCδ, PKCξ, p70 S6 kinase, MSK1 or MSK2
or a fragment or fusion thereof. The polypeptides whose amino acid
sequences are shown above are considered to be serum and glucocorticoid-
induced protein kinases. The SGK2 mRNA is present at highest levels in
liver, kidney and pancreas and is also present in the brain, whereas levels

of mRNA encoding SGK1 and SGK3 are similar in all tissues tested (see Example 5).

By "substantially pure" we mean that the said polypeptide is substantially

5   free of other proteins. Thus, we include any composition that includes at least 30% of the protein content by weight as the said polypeptide, preferably at least 50%, more preferably at least 70%, still more preferably at least 90% and most preferably at least 95% of the protein content is the said polypeptide.

10

Thus, the invention also includes compositions comprising the said polypeptide and a contaminant wherein the contaminant comprises less than 70% of the composition by weight, preferably less than 50% of the composition, more preferably less than 30% of the composition, still more

15   preferably less than 10% of the composition and most preferably less than 5% of the composition by weight.

The invention also includes the substantially pure said polypeptide when combined with other components *ex vivo*, said other components not being

20   all of the components found in the cell in which said polypeptide is found.

SGK, for example the activated or deactivated SGK obtained or obtainable by the above methods of the invention, may be useful, for example in screening methods, such as those set out below. Thus, it will be

25   appreciated that the term SGK as used herein includes a polypeptide comprising an amino acid sequence given above for SGK2 or SGK3 or the amino acid sequence of the polypeptide, preferably a protein kinase, encoded by I.M.A.G.E Consortium clone ID 42669, or a variant, fragment, fusion or derivative thereof, or a fusion of a said variant or

10

fragment or derivative, wherein the said polypeptide is a protein kinase.

It is preferred that the said polypeptide is a protein kinase that is capable

of phosphorylating a polypeptide comprising the consensus Arg-X-

(X/Arg)-X-X-(Ser/Thr)-Z where X indicates any amino acid, X/Arg

indicates any amino acid, with a preference for arginine, and Z indicates

that the amino acid residue is preferably a hydrophobic residue. An

example of such a polypeptide is Crosstide (GRPRTSSFAEG). The

underlined residue may be phosphorylated by the said protein kinase.

Other examples of polypeptides that may be phosphorylated by the said

protein kinase are shown in Table 1 and may include GSK3, as discussed

in Example 1. As discussed in Example 5, serine 279 of SGK2 lies in a

sequence conforming to the consensus sequence for phosphorylation by

SGK and PKB. SGK2 may therefore be capable of being phosphorylated

by the said protein kinase, for example SGK2. It will be appreciated that

the said protein kinase is not PKB (for example, PKBα), p70 S6 kinase,

protein kinase C (for example, PKCδ or PKCζ), MAPKAP kinase-

1(Leighton *et al* (1995) *FEBS Lett* 375, 289-293) or MSK1 or MSK2 (see,

for example, UK patent applications 9817303.2, filed 10 August 1998 and

9813467.9, filed 24 June 1998). As discussed in Example 5, SGK3, for

example, may also be capable of phosphorylating a serine residue

equivalent to serine 77 or serine 79 of full-length human SGK3.

It will be appreciated that a said polypeptide may be useful, for example in

some of the screening assays as set out below, even if it does not possess

protein kinase activity as defined above. It will further be appreciated that

the phosphorylation of such a polypeptide may be detected by means

described herein other than by detecting a change in enzymatic, in

particular protein kinase, activity of the polypeptide.

It is preferred that the SGK comprises an amino acid sequence corresponding to the consensus sequence B-T̲-F-C-G-T-(P/I)-(D/E)-Y-(L/I/M)-A-P-E, where B is a basic residue, the consensus sequence for phosphorylation of a polypeptide by PDK1, and/or the consensus sequence

5   Phe-Xaa-Xaa-(Phe/Tyr)-(Ser/Thr)-(Phe/Tyr), the consensus sequence proposed for phosphorylation of a polypeptide by PDK2 protein kinase activity. Preferably both consensus sequences are present. Alternatively, the Ser/Thr in either consensus sequence may be replaced by an aspartate or glutamate (ie acidic) residue; it is preferred that only one such

10   consensus sequence in a polypeptide is replaced in this way. It is preferred that the Ser/Thr in the consensus sequence for phosphorylation by PDK1 is not replaced in this way; as described in Example 1, replacement of Thr256 to Asp in human SGK1 may abolish activation of SGK.

15

By "variants" of the polypeptide we include insertions, deletions and substitutions, either conservative or non-conservative. In particular we include variants of the polypeptide where such changes do not substantially alter the activity of the said protein kinase.

20

By "conservative substitutions" is intended combinations such as Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

25   It is particularly preferred if the SGK variant has an amino acid sequence which has at least 65% identity with the amino acid sequence of the polypeptide, preferably a protein kinase, encoded by I.M.A.G.E Consortium clone ID 42669, more preferably at least 70%, 71%, 72%, 73% or 74%, still more preferably at least 75%, yet still more preferably

at least 80%, in further preference at least 85%, in still further preference at least 90% and most preferably at least 95% or 97% identity with the amino acid sequence encoded by I.M.A.G.E Consortium clone ID 42669.

5   It is particularly preferred that a SGK2 or SGK3 variant has an amino acid sequence which has at least 65% identity with the amino acid sequence of SGK2 or SGK3, as appropriate, indicated above, more preferably at least 70%, 71%, 72%, 73% or 74%, still more preferably at least 75%, yet still more preferably at least 80%, in further preference at least 85%, in 10   still further preference at least 90% and most preferably at least 95% or 97% identity with the amino acid sequence of SGK2 or SGK3 indicated above.

It is still further preferred if the SGK variant has an amino acid sequence 15   which has at least 65% identity with the amino acid sequence of the catalytic domain of the polypeptide, preferably a protein kinase, encoded by I.M.A.G.E Consortium clone ID 42669, more preferably at least 70%, 71%, 72%, 73% or 74%, still more preferably at least 75%, yet still more preferably at least 80%, in further preference at least 83 or 85%, in still 20   further preference at least 90% and most preferably at least 95% or 97% identity with the amino acid sequence defined above.

It is still further preferred that a SGK2 or SGK3 variant has an amino acid sequence which has at least 65% identity with the amino acid sequence of 25   the catalytic domain of an SGK2 or SGK3 polypeptide whose sequence is indicated above, as appropriate, more preferably at least 70%, 71%, 72%, 73% or 74%, still more preferably at least 75%, yet still more preferably at least 80%, in further preference at least 83 or 85%, in still further

13

preference at least 90% and most preferably at least 95% or 97% identity with the SGK2 or SGK3 amino acid sequence defined above.

It will be appreciated that the catalytic domain of a protein kinase-related

5   polypeptide may be readily identified by a person skilled in the art, for example using sequence comparisons as described below, and as described in relation to SGK in, for example, Webster *et al* (1993) *Mol Cell Biol* 13(4), 2031-2040. For example, as discussed in Example 5, the amino acid sequences of the three SGK isoforms are about 80 % identical to one

10   another in the catalytic domain, while the short C-terminal non-catalytic domains are less similar (44-68 % identity). The N-terminal 85 residues that precede the catalytic domain are much less similar. In this region there is only about 25% identity between SGK1 and SGK3 and almost no identity between SGK2 and the other isoforms (Fig 13).

15

The percent sequence identity between two polypeptides may be determined using suitable computer programs, for example the GAP program of the University of Wisconsin Genetic Computing Group and it

20   will be appreciated that percent identity is calculated in relation to polypeptides whose sequence has been aligned optimally.

The alignment may alternatively be carried out using the Clustal W program (Thompson *et al.*, 1994). The parameters used may be as

25   follows:
Fast pairwise alignment parameters: K-tuple(word) size; 1, window size; 5, gap penalty; 3, number of top diagonals; 5. Scoring method: x percent. Multiple alignment parameters: gap open penalty; 10, gap extension penalty; 0.05.

14

Scoring matrix: BLOSUM.

It will be appreciated that SGK2 and SGK3, as defined above by their amino acid sequence, are examples of SGK variants as defined above.

5

It is preferred that the SGK is a polypeptide which consists of the amino acid sequence of the protein kinase encoded by I.M.A.G.E Consortium clone ID 42669, or SGK2 or SGK3, the amino acid sequences of which are given above, or naturally occurring allelic variants (including splice

10   variants) thereof.

It is also preferred that the SGK is one of the following:

(1) a polypeptide encoded by I.M.A.G.E Consortium clone ID 42669 (SGK1) or SGK2 or SGK3 as defined above lacking the amino acids

15   equivalent to the N-terminal 60 amino acids of full-length human SGK1 (for example ΔN-SKG(61-431) as described in Example 1 or SGK2α as described in Example 5 and shown in Figure 13)

(2) full-length SGK or SGK lacking the N-terminal 60 amino acids, as described above, in which the residue equivalent to serine 422 of full-

20   length SGK1 is replaced by aspartate or glutamate (preferably aspartate) and/or the residue equivalent to threonine 256 of full-length SGK1 is replaced by aspartate or glutamate or alanine

(3) a fusion polypeptide of glutathione-S-transferase (GST) and any of the variants of SGK described above, for example a fusion protein comprising

25   the GST encoded by the GST sequence of the plasmid pEBG2T, as known to those skilled in the art. Examples include GST-ΔN-SGK[S422D], as described in Example 1.

15

It will be appreciated that SGK in which the residue equivalent to threonine 256 of full-length SGK1 is replaced, for example by an alanine, glutamate or aspartate residue, may not be capable of being significantly activated by phosphorylation and may therefore be less preferred than

5   some other SGKs for use in the screening methods of the invention. Thus, GST-SGK[T256D], GST-SGK[T256E], GST-SGK[T256A], as described in Example 1, may not be capable of being significantly activated by phosphorylation and may therefore be less preferred than some other SGKs for use in the screening methods of the invention.

10

As discussed in Example 5, the residue equivalent to serine 422 of SGK1 in SGK2α is serine 356 and in SGK3 is serine 419. The residue equivalent to threonine 256 of SGK1 in SGK2α is threonine 193 and in SGK3 is threonine 253.

15

It will further be appreciated that SGK in which the residue equivalent to serine 422 of full-length SGK1 is replaced by an amino acid residue other than glutamate or aspartate (ie an acidic residue) or a residue that may be phosphorylated, for example by an alanine residue, may not be capable of

20   being activated by phosphorylation or may be less capable of being activated by phosphorylation than SGK in which the said residue equivalent to serine 422 is not so replaced.

It will be appreciated that a mutated SGK which does not have any protein

25   kinase activity ("kinase dead" mutant) may be phosphorylated in a similar manner to SGK that does have protein kinase activity, but that no change in protein kinase activity may be discernible. Such a mutated SGK may be SGK in which the residue equivalent to lysine 127 of full-length SGK1

(which may lie in the ATP binding site) is replaced by alanine, as described in Example 1.

SGK (as defined above) may be phosphorylated by phosphatidylinositol dependent kinase 1 (PDK1), or a variant, fragment, fusion or derivative thereof, or a fusion of a said variant, fragment or derivative. The term PDK1 is well known to those skilled in the art (see, for example, references 7 to 9) and includes, in particular, PDK1 as described and expressed in reference 9 and in co-pending application PCT/GB98/00777. It is preferred that the said variant, fragment, fusion or derivative of PDK1, or a fusion of a said variant, fragment or derivative is a protein kinase, preferably a protein kinase capable of phosphorylating a polypeptide comprising an amino acid sequence corresponding to the consensus sequence B-$\underline{T}$-F-C-G-T-(P/I)-(D/E)-Y-(L/I/M)-A-P-E. Such variants of PDK1 may be functional equivalents of PDK1 and include Pkh1 and Pkh2 from *Saccharomyces cerevisiae* as described in the US patent application entitled "Screening Methods" filed on the same day as this application.

SGK may be dephosphorylated by a serine/threonine protein phosphatase, for example PP1 (Berndt *et al* (1987) *FEBS Lett* 223, 340-346), PP2C (Mann *et al* (1992) *Biochem et Biophys Acta* 1130, 100-104 or protein phosphorylase 2A (PP2A; da Cruz E Silva (1987) *FEBS Lett* 221, 415-422) or a variant, fragment, fusion or derivative any thereof, or a fusion of a said variant, fragment or derivative. PP1, PP2C or PP2A or a variant, fragment, fusion or derivative any thereof, or a fusion of a said variant, fragment or derivative is capable of dephosphorylating phosphorylase *a*. The terms PP1, PP2C, PP2A and phosphorylase *a* are

17

well known to those skilled in the art.   PP2A may be inactivated by
microcystin-LR at 1 μM.

A further aspect of the invention is the use of a serine/threonine protein

5   phosphatase, for example PP1, PP2C, PP2A or a variant, fragment,
fusion or derivative any thereof, or a fusion of a said variant, fragment or
derivative (as defined above) in a method of deactivating and/or
dephosphorylating SGK.   The SGK may be phosphorylated SGK, as
discussed above.

10

A still further aspect of the invention is the use of a protein kinase,
preferably PDK1 or a variant, fragment, fusion or derivative thereof, or a
fusion of a said variant, fragment or derivative (as defined above) in a
method of activating and/or phosphorylating SGK.   The SGK may be

15   dephosphorylated SGK, as discussed above.

A further aspect of the invention is a method of activating SGK (as defined
above) wherein SGK is phosphorylated on the residue equivalent to
Thr256 of full-length human SGK1.   SGK (for example full-length human

20   SGK and ΔN-SGK(61-431), may be phosphorylated on the residue
equivalent to Thr 256 of full-length human SGK1 by PDK1.   SGK may be
activated by phosphorylation on this residue, as described in Example 1
and Example 5.   It will be appreciated that SGK in which the residue
equivalent to serine 422 of full-length SGK1 is replaced by an acidic

25   residue, for example glutamate or aspartate, may be more readily
phosphorylated and/or activated than SGK in which the said residue
equivalent to serine 422 is not so replaced.   For example, recombinant
SGK in which the residue equivalent to serine 422 of full-length SGK1 is
replaced by an acidic residue, for example glutamate or aspartate, may be

substantially phosphorylated on the residue equivalent to Thr256 of full-length human SGK1 when expressed in a eukaryotic, preferably mammalian, cell. Such recombinant SGK may be useful in screening assays in which activated SGK is required, as discussed further below.

5

It will be appreciated that a protein kinase capable of phosphorylating SGK on the residue equivalent to Thr256 of full-length human SGK1 may be identified by determining whether any particular protein kinase is capable of activating SGK and/or determining what, if any residue of SGK

10   may be phosphorylated by the said particular protein kinase, for example as described in Example 1.

By "residue equivalent to Thr256 of full-length human SGK1", for example, is included the meaning that the amino acid residue that occupies

15   a position in the native three dimensional structure of a protein kinase corresponding to the position occupied by Thr 256 in the native three dimensional structure of human full-length SGK1. It will be appreciated that Thr256 of human full-length SGK1 is located in the "activation loop" between subdomains VII and VIII of the catalytic domain.

20

Protein kinases show a conserved catalytic core, as reviewed in Johnson *et al* (1996) *Cell*, **85**, 149-158 and Taylor & Radzio-Andzelm (1994) *Structure* **2**, 345-355. This core folds into a small N-terminal lobe largely comprising anti-parallel β-sheet, and a large C-terminal lobe which is

25   mostly α-helical.

The residue equivalent to, for example, Thr 256 of full-length human SGK1 may be identified by alignment of the sequence of the polypeptide with that of full-length human SGK1 in such a way as to maximise the

19

match between the sequences. The alignment may be carried out by visual inspection and/or by the use of suitable computer programs, for example the GAP program of the University of Wisconsin Genetic Computing Group, which will also allow the percent identity of the polypeptides to be

5   calculated. The Align program (Pearson (1994) in: Methods in Molecular Biology, Computer Analysis of Sequence Data, Part II (Griffin, AM and Griffin, HG eds) pp 365-389, Humana Press, Clifton). Thus, residues identified in this manner are also "equivalent residues".

10   It will be appreciated that in the case of truncated forms of SGK or in forms where simple replacements of amino acids have occurred it is facile to identify the "equivalent residue".

The sequence for human SGK1 is given, for example, in Webster *et al*

15   (1993) *Mol cell Biol* 13(4), 2031-2040.

It will be appreciated that identification of the residue equivalent to Thr 256, for example, may depend on the alignment of surrounding conserved residues.

20

A further aspect of the invention is a method of activating SGK (as defined above) wherein SGK is phosphorylated on the residue equivalent to Ser422 of full-length human SGK. SGK (for example full-length human SGK and ΔN-SGK(61-431), may be phosphorylated on the residue equivalent to Ser

25   422 of full-length human SGK1 by a preparation containing PDK2 activity. SGK may be activated by phosphorylation on this residue, as described in Example 1. The method may be performed in a cell, for example a mammalian cell that is stimulated by, for example, IGF-1 and/or hydrogen peroxide. The method may comprise culturing a host

20

cell comprising a recombinant polynucleotide or a replicable vector which encodes SGK, stimulating the cell, for example with IGF-1 and/or hydrogen peroxide and isolating said polypeptide from said host cell. Methods of cultivating host cells and isolating recombinant proteins are

5   well known in the art.

The residue equivalent to Ser422 or other residue of full-length human SGK1 may be identified by methods analagous to those described above for the residue equivalent to Thr256 of full-length human SGK1. Ser422

10   of human full-length SGK1 lies towards the C-terminus of the polypeptide.

A preparation containing PDK2 activity may phosphorylate polypeptides comprising an amino acid sequence corresponding to the consensus sequence Phe-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr.

15

SGK may be phosphorylated on the residue equivalent to Ser422 of full-length human SGK1, for example *in vitro*, by a protein kinase that may not have the physiological characteristics of PDK2 or may not require the consensus sequence thought to be required by PDK2. Thus, *in vitro*, SGK

20   may be phosphorylated by a protein kinase that may not phosphorylate SGK in a physiologically relevant manner *in vivo* and may not correspond to an activity identified as PDK2.   This may be analagous to the phosphorylation *in vitro* of PKBα on the site equivalent to Ser422 of SGK (Ser473) by MAPKAP Kinase-2 (Alessi *et al* (1996) *EMBO J* 15, 6541-

25   6551).   MAPKAP Kinase-2 does not require the consensus sequence identified as required by PDK2.

It will be appreciated that a protein kinase that is capable of phosphorylating the residue equivalent to Ser422 of full-length human

21

SGK1 may be identified by methods similar to those described above and in Example 1 for identifying a protein kinase that may phosphorylate the residue equivalent to Thr256 of full-length human SGK1.

5   The phosphorylation of SGK may be PtdIns(3,4,5)P$_3$ dependent. In particular, the phosphorylation of the residue equivalent to Ser422, for example by a preparation containing PDK2 activity, may be PtdIns(3,4,5)P$_3$ dependent. Thus, *in vivo*, the phosphorylation of the residue equivalent to Ser422 may be dependent upon the activity of PtdIns

10   3-kinase.

The phosphorylation of SGK on the residue equivalent to Thr256 of full-length human SGK1 may be dependent upon the phosphorylation of the residue equivalent to Ser 422 of full-length human SGK1. Alternatively,

15   if serine 422 is replaced by an aspartate residue, as described in Examples 1 and 5, then the phosphorylation of the residue equivalent to Thr256, for example by PDK1, may be potentiated. Thus, the phosphorylation of Thr256 may require that (or be enhanced if) the residue equivalent to Ser422 is phosphorylated or is replaced by an aspartate residue.

20

As discussed in Example 5, SGK2 may be phosphorylated at residues Ser279 and/or Ser334. Ser279 may be phosphorylated by SGK, for example SGK2, or PKB. It may be necessary for the SGK, for example SGK2, or PKB to be activated, for example by phosphorylation by PDK1.

25   Ser334 may be phosphorylated by PDK1. SGK3 may be phosphorylated at residues Ser77 and/or Ser79. These residues may be phosphorylated by SGK, for example SGK3, or PKB. It may be necessary for the SGK, for example SGK3, or PKB to be activated, for example by phosphorylation

22

by PDK1 but phosphorylation of Ser77 and Ser79 of SGK3 may take place in the absence of phosphorylation by PDK1.

A further aspect of the invention is a fusion polypeptide of SGK or a variant, fragment or derivative thereof. The fusion polypeptide may comprise, for example, a fragment of SGK or variant or derivative thereof wherein the residues equivalent to the N-terminal about 20, 30, 40, 50 or 60 amino acids of human full-length SGK1 are deleted. The fusion polypeptide may further comprise glutathione-S-transferase. The glutathione-S-transferase may be fused to the N-terminus or C-terminus of SGK or the said fragment variant or derivative thereof; preferably it is fused to the N-terminus, for example as shown in Examples 1 and 5.

It is particularly preferred that the fusion polypeptide has at least 5%, 10%, 15%, 20%, 25% or 30% of the enzyme activity of SGK, for example SGK1, with respect to the phosphorylation of Crosstide (GRPRTSSFAEG; see Example 1). It is more preferred if the fusion polypeptide has at least 50%, preferably at least 70% and more preferably at least 90% of the enzyme activity of SGK with respect to the phosphorylation of Crosstide. It is preferred that the fusion polypeptide comprises the residue equivalent to Thr256 and/or the residue equivalent to Ser 422 of full-length human SGK1. It will be appreciated that a fusion polypeptide with low enzymic activity may be useful in applications including high throughput screening, for example if it is expressed in high amounts or may be easily purified or stored. However, it will be appreciated that fusion polypeptides which are devoid of enzymatic activity may nevertheless also be useful, for example by interacting with another polypeptide, or as antigens in raising antibodies, or the phosphorylation of such variants or fusions or derivatives or fragments

23

may be measured. It will be appreciated that fusions of PKBα, PKCδ, PKCξ, p70 S6 kinase, MSK1 and MSK2 are not polypeptides of the invention, unless they include all or part of SGK.

5   A further aspect of the invention is a polypeptide comprising the amino acid sequence of human SGK or a fragment, variant, derivative or fusion thereof wherein the residue equivalent to serine 422 of full-length human SGK1 is replaced (for example by an aspartate, glutamate or alanine residue) and/or the residue equivalent to threonine 256 of full-length

10   human SGK1 is replaced (for example by an alanine residue), and/or the residue equivalent to lysine 127 of full-length human SGK1 is replaced (for example by an alanine residue). The residue equivalent to lysine 127 of full-length human SGK1 may be identified in a manner analogous to that described above for the residue equivalent to serine 422, and may lie

15   in the ATP binding site. The residue equivalent to serine 422 of full-length human SGK1 may be replaced by a residue that is capable of carrying a negative charge (for example an aspartate or glutamate residue), which may mimic the effect of phosphorylation of serine 422. Alternatively, the residue equivalent to serine 422 of full-length human

20   SGK1 may be replaced by a residue, for example alanine, that cannot be phosphorylated and is not capable of carrying a negative charge, and preferably is of a similar bulk to serine or threonine. The residue equivalent to threonine 256 of full-length human SGK1 may similarly be replaced by a residue that is capable of carrying a negative charge (for

25   example an aspartate or glutamate residue), or by a residue, for example alanine, that cannot be phosphorylated and is not capable of carrying a negative charge and preferably is of a similar bulk to serine or threonine. The residue equivalent to lysine 127 of full-length human SGK1 may be

replaced by a residue that is not capable of carrying a positive charge, for example an alanine residue.

It is preferred that the residue equivalent to serine 422 of full-length
5   human SGK1 is replaced by an aspartate residue and the residues equivalent to threonine 256 and lysine 127 of the full-length human SGK1 are unmutated, ie are threonine and lysine respectively. It is further preferred that the amino acids equivalent to the N-terminal 20, 30, 40, 50 or 60 amino acids of full-length human SGK1 are not present, ie are
10   deleted in relation to SGK1, SGK2β or SGK3. It will be appreciated that human SGK2α does not have an amino acid sequence equivalent to the N-terminal 60 amino acids of full-length human SGK1. It will further be appreciated that this may have the consequence that the interaction with a cellular component may not be the same for human SGK2α as for other
15   SGKs, for example SGK1, SGK2β or SGK3.

SGK2 is capable of being phosphorylated at Ser279 and Ser334, as well as Thr193. Thus, it may alternatively or additionally be preferred that the residue equivalent to Ser279 and/or Ser334 of full length SGK2 is
20   replaced by a residue that is capable of carrying a negative charge (for example an aspartate or glutamate residue), or by a residue, for example alanine, that cannot be phosphorylated and is not capable of carrying a negative charge and preferably is of a similar bulk to serine or threonine.

25   SGK3 is capable of being phosphorylated at Ser77 and Ser79. Thus, it may alternatively or additionally be preferred that the residue equivalent to Ser77 and/or Ser79 of full length SGK3 is replaced by a residue that is capable of carrying a negative charge (for example an aspartate or

glutamate residue), or by a residue, for example alanine, that cannot be phosphorylated and is not capable of carrying a negative charge and preferably is of a similar bulk to serine or threonine.

5   It will be appreciated that phosphorylation of SGK2 at Ser279 and/or Ser334 or phosphorylation of SGK3 at Ser77 and/or Ser79 may modulate the activity or, for example, the cellular location of SGK2 or SKG3.

       It will be appreciated that a polypeptide comprising the amino acid
10   sequence of human SGK or a fragment, variant, derivative or fusion thereof wherein the residue equivalent to threonine 256 of full-length human SGK1 is replaced by an alanine residue, and/or the residue equivalent to lysine 127 of full-length human SGK1 is replaced by an alanine residue may not be capable of being activated by phosphorylation
15   and/or may be devoid of protein kinase activity, respectively, and therefore may not be useful in screening methods of the invention.

       A further aspect of the invention is a polynucleotide encoding a polypeptide of the invention, for example encoding SGK2 or SGK3 or
20   encoding a variant or fragment or derivative of fusion of said SGK2 or SGK3 or a fusion of a said variant or fragment or derivative. Preferences and exclusions for the said polynucleotide variant are the same as in the first aspect of the invention, except that the following Expressed Sequence Tags (ESTs) are also excluded:

25   The polynucleotide may be a recombinant polynucleotide. The following Expressed Sequence Tags (ESTs) are excluded:

       AA130828 (IMAGE Consortium, St Louis, MO, USA); AI386362; AA790370; AA138663; AA219166 (related to SGK2)

AA219166 (related to SGK3).

All ESTs are identified by the Genbank accession number, as described in
Examples 1 and 5.

5

The polynucleotide may be a vector suitable for replication and/or
expression of the polypeptide in a mammalian/eukaryotic cell.

A still further aspect of the invention is a recombinant polynucleotide
10   suitable for expressing a polypeptide of the invention. It is not considered
that any of the ESTs listed above are polynucleotides as defined above;
however, for the avoidance of doubt, the ESTs excluded above are further
excluded from this aspect of the invention.

15   The polynucleotide or recombinant polynucleotide may be DNA or RNA,
preferably DNA. The polynucleotide may or may not contain introns in
the coding sequence; preferably the polynucleotide is or comprises a
cDNA.

20   In one preferred embodiment the polynucleotide comprises the nucleotide
sequence

```
      GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGG
      AGTTTTCAGAGCTGCCTGATCATTGCTACAGAATGAACTCTAGCCCAGCTGGGAC
      CCCAAGTCCACAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCC
25    AACCCAAATGCCCAGCCCACGGACTTCGACTTCCTCAAAGTCATCGGCAAAGGGA
      ACTACGGGAAGGTCCTACTGGCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGT
      GAAGGTACTACAGAAAAAGTCCATCTTAAAGAAGAAAGAGCAGAGCCACATCATG
      GCAGAGCGCAGTGTGCTTCTGAAGAACGTGCGGCACCCCTTCCTCGTGGGCCTGC
      GCTACTCCTTCCAGACACCTGAGAAGCTCTACTTCGTGCTCGACTATGTCAACGG
30    GGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCC
      AGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCACTCCCTCAACA
      TCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGACACGT
      GGTGCTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA
      TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGC
35    CTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGTCCTCTACGAGATGCT
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      CCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATT
      CTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCC
      TGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
      TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTAC
  5   CACAAGAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGA
      AGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTAC
      CCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCATTCCTGGGATTTTCT
      TATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGGACCTGTGAAA
      CTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAAGAGCG
 10   ACTCAAACTAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA
      AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCA
      GAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTG
      CTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAA
      ATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAAGCT
 15   CCCCCCAATGACTTTTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
      AGGCTGGGAAATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGG
      GGTTTTGACCCTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCCCTCTTT
      TACCATAGGGCCTCCTGGTGTTTGGATTTTGATCTCAATGTGTAAAATGACAGAG
      ATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTCTATGTTGAAAAAAAA
 20   AAAAAAAAAAAAAAAAAAAA

      or

      ATGGGTTCAGACTTTATGCCCTGAAAAGATCCTTCCAGCCCTGGCCATCTTGGAC
      TTCTGGAGCTACCCTGGCTCACAGGGGTCTTGTTGCCCTGGGTGTCCCCAGTTCT
 25   TGAAAAGAATCAGCCTGGGAGGGGCCACACCCTGACCATCCCCCTTTATCCCTTC
      TGAGATGTTTGTTAGGAAGTCTGGGTCCAGGGGATATCATTTCTTGTTCCATCCA
      TGCAGGGGTTGCTTACCTCGGGTAGGAAACCCTCAGGCGGTGGCAGGTGCACAGG
      TAGGGGAGGATGGAGAGGGCAGTGGTGCCTGAAGCCCTGGATGGGCGGAGCTGAC
      CCCCCAACACCAACTCTATCATGCCTGCTCCTCCCTGTCCCCCCAGAGCTGCCTG
 30   ATCATTGCTACAGAATGAACTCTAGCCCAGCTGGGACCCCAAGTCCACAGCCCTC
      CAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCCAGCCC
      ACGGACTTCGACTTCCTCAAAGTCATCGGCAAAGGGAACTACGGGAAGGTCCTAC
      TGGCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAA
      GTCCATCTTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTT
 35   CTGAAGAACGTGCGGCACCCCTTCCTCGTGGGCCTGCGCTACTCCTTCCAGACAC
      CTGAGAAGCTCTACTTCGTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCA
      CCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAG
      GTGGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGA
      AACCAGAGAACATTCTCTTGGACTGCCAGGGACACGTGGTGCTGACGGATTTTGG
 40   CCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACC
      CCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGG
      ACTGGTGGTGCTTGGGGGCAGTCCTCTACGAGATGCTCCATGGCCTGCCGCCCTT
      CTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTACAG
      ATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACA
 45   AGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCA
      TGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCA
      CCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGT
      TCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAG
      CAGCTCTGGGGCCTCAAGTGCATTCCTGGGATTTTCTTATGCGCCAGAGGATGAT
 50   GACATCTTGGATTGCTAGAAGAGAAGGACCTGTGAAACTACTGAGGCCAGCTGGT
      ATTAGTAAGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACTAACAATGGC
      TTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCG
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28

GAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCC
TGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATGGTTACTGG
AGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGAGAA
GAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAAGCTCCCCCCAATGACTTTTGC
5 TTCCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCT
TATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACA
TTAGGGGAGAATGTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGG
TGTTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCATAGG
GTATCAATATCTCTTATTGTTCTATGTTGAAAAAAAAAAAAAAAAAAAAAAAAAA
10 A

or a variant, fragment, fusion or derivative thereof. The first nucleotide

sequence encodes SGK2α and the second encodes SGK2β. The nucleotide

sequences are shown in Figure 1 together with the translations of the

relevant open reading frames.

15

In another preferred embodiment the polynucleotide comprises the

nucleotide sequence

GGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACTACAAG
20 GAAAGCTGCCCAAGTGTAAGCATTCCCAGCTCCGATGAACACAGAGAGAAA
AAGAAGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAA
TGGTTTGTCTTCAGGAGATATGCAGAGTTTGATAAACTTTATAACACTTTA
AAAAAACAGTTTCCTGCTATGGCCCTGAAGATTCCTGCCAAGAGAATATTT
GGTGATAATTTTGATCCAGATTTTATTAAACAAAGACGAGCAGGACTAAAC
25 GAATTCATTCAGAACCTAGTTAGGTATCCAGAACTTTATAACCATCCAGAT
GTCAGAGCATTCCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCATCT
GAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAAC
ATCAACCTGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGAT
TTCTTAAAAGTTATTGGAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAA
30 CGGAAACTGGATGGAAAATTTTATGCTGTCAAAGTGTTACAGAAAAAAATA
GTTCTCAACAGAAAAGAGCAAAAACATATTATGGCTGAACGTAATGTGCTC
TTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATTCCTTCCAA
ACAACTGAAAAGCTTTATTTTGTTCTGGATTTTGTTAATGGAGGGGAGCTT
TTTTTCCACTTACAAAGAGAACGGTCCTTTCCTGAGCACAGAGCTAGGTTT
35 TACGCTGCTGAAATTGCTAGTGCATTGGGTTACTTACATTCCATCAAAATA
GTATACAGAGACTTGAAACCAGAAAATATTCTTTTGGATTCAGTAGGACAT
GTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGAC
ACCACTACCACATTTTGTGGGACACCAGAGTATCTTGCACCTGAAGTAATT
AGAAACAGCCCTATGACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTT
40 CTGTATGAAATGCTGTATGGATTGCCTCCTTTTTATTGCCGAGATGTTGCT
GAAATGTATGACAATATCCTTCACAAACCCCTAAGTTTGAGGCCAGGAGTG
AGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAGACAGGCAA
AATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTT
TTTGAATCACTCAGCTGGGCTGACCTTGTACAAAGAAGATTCCACCACCA
45 TTTAATCCTAATGTGGCTGGACCAGATGATATCAGAAACTTTGACACAGCA

29

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TTTACAGAAGAAACAGTTCCATATTCTGTGTGTGTATCTTCTGACTATTCT
ATAGTGAATGCCAGTGTATTGGAGGCAGATGATGCATTCGTTGGTTTCTCT
TATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAGTTTGCCATTCAGAA
ACCATTGAGCAAAATAAGTCTATAGATGGGACTGAAACTTCTATTTGTGTGA
ATATATTCAAATATGTATAACTAGTGCCTCATTTTTATATGTAATGATGAAAACT
ATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCT
GTTTTGATTAAAATTTATATTCTTGTTTAATAAGCTTATTTTTAAACAATTTAAA
AGCTATTATTCTTAGCATTAACCTATTTTTAAAGAAACCTTTTTTGCTATTGACT
GTTTTTTCCCTCTAAGTTTACACTAACATCTACCCAAGATAGACTGTTTTTTAAC
AGTCAATTTCAGTTCAGCTAACATATATTAATACCTTTGTAACTCTTTGCTATGG
CTTTTGTTATCACACCAAAACTATGCAATTGGTACATGGTTGTTTAAGAAGAAAC
CGTATTTTTCCATGATAAATCACTGTTTGAAATATTTGGTTCATGGTATGATCGA
AATGTAAAAGCATAATTAACACATTGGCTGCTAGTTAACAATTGGAATAACTTTA
TTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGTGGCTCACGCCTGTAAT
CCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCAGGAGTTGGAGA
CCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAATTGGCAG
GGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGAA
TCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACT
CCTGCCTGGGCAACAAGAGTGAAACTCCATCTCCAAAAAAAAAAAAAAAAAA
```

or a variant, fragment, fusion or derivative thereof. The nucleotide

sequence encodes SGK3 and is shown in Figure 2 together with the

translation of the relevant open reading frame.

Site-directed mutagenesis or other techniques can be employed to create

single or multiple mutations, such as replacements, insertions, deletions,

and transpositions, as described in Botstein and Shortle, "Strategies and

Applications of *In Vitro* Mutagenesis," *Science*, **229:** 193-210 (1985),

which is incorporated herein by reference. Polymerase chain reaction

based methods of site-directed mutagenesis may be used, as well known to

those skilled in the art, for example as described in Example 1.

By "suitable for expressing" is mean that the polynucleotide is a

polynucleotide that may be translated to form the polypeptide, for example

RNA, or that the polynucleotide (which is preferably DNA) encoding the

polypeptide of the invention is inserted into an expression vector, such as

a plasmid, in proper orientation and correct reading frame for expression.

The polynucleotide may be linked to the appropriate transcriptional and

translational regulatory control nucleotide sequences recognised by any desired host; such controls may be incorporated in the expression vector.

Characteristics of vectors suitable for replication in mammalian/eukaryotic cells are well known to those skilled in the art, and examples are given below. It will be appreciated that a vector may be suitable for replication in both prokaryotic and eukaryotic cells.

A variety of methods have been developed to operably link polynucleotides, especially DNA, to vectors for example *via* complementary cohesive termini. Suitable methods are described in Sambrook *et al* (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

A desirable way to modify the DNA encoding a polypeptide of the invention is to use the polymerase chain reaction as disclosed by Saiki *et al* (1988) *Science* 239, 487-491. This method may be used for introducing the DNA into a suitable vector, for example by engineering in suitable restriction sites, or it may be used to modify the DNA in other useful ways as is known in the art.

In this method the DNA to be enzymatically amplified is flanked by two specific primers which themselves become incorporated into the amplified DNA. The said specific primers may contain restriction endonuclease recognition sites which can be used for cloning into expression vectors using methods known in the art.

The DNA (or in the case of retroviral vectors, RNA) is then expressed in a suitable host to produce a polypeptide comprising the compound of the

31

invention. Thus, the DNA encoding the polypeptide constituting the compound of the invention may be used in accordance with known techniques, appropriately modified in view of the teachings contained herein, to construct an expression vector, which is then used to transform

5   an appropriate host cell for the expression and production of the polypeptide of the invention. Such techniques include those disclosed in US Patent Nos. 4,440,859 issued 3 April 1984 to Rutter *et al*, 4,530,901 issued 23 July 1985 to Weissman, 4,582,800 issued 15 April 1986 to Crowl, 4,677,063 issued 30 June 1987 to Mark *et al*, 4,678,751 issued 7

10 July 1987 to Goeddel, 4,704,362 issued 3 November 1987 to Itakura *et al*, 4,710,463 issued 1 December 1987 to Murray, 4,757,006 issued 12 July 1988 to Toole, Jr. *et al*, 4,766,075 issued 23 August 1988 to Goeddel *et al* and 4,810,648 issued 7 March 1989 to Stalker, all of which are incorporated herein by reference.

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The DNA (or in the case of retroviral vectors, RNA) encoding the polypeptide constituting the compound of the invention may be joined to a wide variety of other DNA sequences for introduction into an appropriate host. The companion DNA will depend upon the nature of the host, the

20 manner of the introduction of the DNA into the host, and whether episomal maintenance or integration is desired.

Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression.

25 If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognised by the desired host, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Generally, not all of the hosts will be transformed by

32

the vector. Therefore, it will be necessary to select for transformed host cells. One selection technique involves incorporating into the expression vector a DNA sequence, with any necessary control elements, that codes for a selectable trait in the transformed cell, such as antibiotic resistance. Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

Host cells that have been transformed by the recombinant DNA of the invention are then cultured for a sufficient time and under appropriate conditions known to those skilled in the art in view of the teachings disclosed herein to permit the expression of the polypeptide, which can then be recovered.

It will be appreciated that the host cell, for example a mammalian cell such as 293 cells as described in Example 1 or Example 5, may be stimulated, for example using IGF-1 of hydrogen peroxide, such that the SGK polypeptide may be phosphorylated and/or activated in the host cell. The activated SGK polypeptide may then be recovered, if necessary in the presence of phosphatase inhibitors, for example microcystin, for example as described in Example 1. Recovery may entail purification on glutathione-Sepharose, as described in Example 1.

293 cells are human transformed primary embryonal kidney cells that may be obtained from the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852-1776; catalogue reference ATCC CRL 1573.

Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts (for example *Saccharomyces cerevisiae*),

33

filamentous fungi (for example *Aspergillus*), plant cells, animal cells and insect cells.

The vectors include a prokaryotic replicon, such as the ColE1 *ori*, for propagation in a prokaryote, even if the vector is to be used for expression in other, non-prokaryotic, cell types. The vectors can also include an appropriate promoter such as a prokaryotic promoter capable of directing the expression (transcription and translation) of the genes in a bacterial host cell, such as *E. coli*, transformed therewith.

A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with exemplary bacterial hosts are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention.

Typical prokaryotic vector plasmids are pUC18, pUC19, pBR322 and pBR329 available from Biorad Laboratories, (Richmond, CA, USA) and p*Trc*99A and pKK223-3 available from Pharmacia, Piscataway, NJ, USA.

A typical mammalian cell vector plasmid is pSVL available from Pharmacia, Piscataway, NJ, USA. This vector uses the SV40 late promoter to drive expression of cloned genes, the highest level of expression being found in T antigen-producing cells, such as COS-1 cells.

An example of an inducible mammalian expression vector is pMSG, also available from Pharmacia. This vector uses the glucocorticoid-inducible promoter of the mouse mammary tumour virus long terminal repeat to drive expression of the cloned gene.

Useful yeast plasmid vectors are pRS403-406 and pRS413-416 and are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Plasmids pRS403, pRS404, pRS405 and pRS406 are Yeast

5   Integrating plasmids (YIps) and incorporate the yeast selectable markers *HIS3*, *TRP1*, *LEU2* and *URA3*. Plasmids pRS413-416 are Yeast Centromere plasmids (YCps).

The present invention also relates to a host cell transformed with a

10   polynucleotide vector construct of the present invention. The host cell can be either prokaryotic or eukaryotic. Bacterial cells are preferred prokaryotic host cells and typically are a strain of *E. coli* such as, for example, the *E. coli* strains DH5 available from Bethesda Research Laboratories Inc., Bethesda, MD, USA, and RR1 available from the

15   American Type Culture Collection (ATCC) of Rockville, MD, USA (No ATCC 31343). Preferred eukaryotic host cells include yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human fibroblastic cell line. Yeast host cells include YPH499, YPH500 and YPH501 which are generally available from

20   Stratagene Cloning Systems, La Jolla, CA 92037, USA. Preferred mammalian host cells include human embryonic kidney 293 cells (see Example 1), Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH/3T3 available from the ATCC as CRL 1658, and monkey kidney-derived COS-1 cells available

25   from the ATCC as CRL 1650. Preferred insect cells are Sf9 cells which can be transfected with baculovirus expression vectors.

Transformation of appropriate cell hosts with a DNA construct of the present invention is accomplished by well known methods that typically

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depend on the type of vector used. With regard to transformation of prokaryotic host cells, see, for example, Cohen *et al* (1972) *Proc. Natl. Acad. Sci. USA* 69, 2110 and Sambrook *et al* (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring

5   Harbor, NY. Transformation of yeast cells is described in Sherman *et al* (1986) *Methods In Yeast Genetics, A Laboratory Manual*, Cold Spring Harbor, NY. The method of Beggs (1978) *Nature* 275, 104-109 is also useful. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome

10   formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, MD 20877, USA.

Electroporation is also useful for transforming and/or transfecting cells and is well known in the art for transforming yeast cell, bacterial cells,

15   insect cells and vertebrate cells.

For example, many bacterial species may be transformed by the methods described in Luchansky *et al* (1988) *Mol. Microbiol.* 2, 637-646 incorporated herein by reference. The greatest number of transformants is

20   consistently recovered following electroporation of the DNA-cell mixture suspended in 2.5X PEB using 6250V per cm at 25:FD.

Methods for transformation of yeast by electroporation are disclosed in Becker & Guarente (1990) *Methods Enzymol.* 194, 182.

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Successfully transformed cells, ie cells that contain a DNA construct of the present invention, can be identified by well known techniques. For example, cells resulting from the introduction of an expression construct of the present invention can be grown to produce the polypeptide of the

36

invention. Cells can be harvested and lysed and their DNA content examined for the presence of the DNA using a method such as that described by Southern (1975) *J. Mol. Biol.* 98, 503 or Berent *et al* (1985) *Biotech.* 3, 208. Alternatively, the presence of the protein in the

5   supernatant can be detected using antibodies as described below.

In addition to directly assaying for the presence of recombinant DNA, successful transformation can be confirmed by well known immunological methods when the recombinant DNA is capable of directing the expression

10   of the protein. For example, cells successfully transformed with an expression vector produce proteins displaying appropriate antigenicity. Samples of cells suspected of being transformed are harvested and assayed for the protein using suitable antibodies.

15   Thus, in addition to the transformed host cells themselves, the present invention also contemplates a culture of those cells, preferably a monoclonal (clonally homogeneous) culture, or a culture derived from a monoclonal culture, in a nutrient medium.

20   A further aspect of the invention provides a method of making the polypeptide of the invention the method comprising culturing a host cell comprising a recombinant polynucleotide or a replicable vector which encodes said polypeptide, and isolating said polypeptide from said host cell. Methods of cultivating host cells and isolating recombinant proteins

25   are well known in the art.

A still further aspect of the invention provides a method of making and activating the polypeptide of the invention the method comprising culturing a host cell, preferably a eukaryotic cell, comprising a

recombinant polynucleotide or a replicable vector which encodes said polypeptide, stimulating the cell, for example with IGF-1 and/or hydrogen peroxide and isolating said polypeptide from said host cell. Methods of cultivating host cells and isolating recombinant proteins are well known in the art. The host cell may be a mammalian cell that is stimulated by, for example, IGF-1 and/or hydrogen peroxide, for example a 293 cell.

A further aspect of the invention is a polypeptide obtainable by the above methods of the invention.

A still further aspect of the invention is a method of identifying a compound that modulates the activity of SGK wherein activated SGK is used.

A further aspect of the invention is the use of activated SGK in a screening assay for a drug-like compound or lead compound for the development of a drug-like compound. It will be appreciated that by a drug-like compound or lead compound for the development of a drug-like compound are included compounds that may be useful in medicine and compounds that may be useful in the development of a compound that may be useful in medicine. Examples of such screening assays may include the methods of the invention described below.

A further aspect of the invention is a method of identifying a compound that modulates the activity of SGK (as defined above), the method comprising contacting a compound with SGK and determining whether the activity of the said polypeptide is changed compared to the activity of the said SGK in the absence of said compound wherein the activity of SGK is measured by measuring the phosphorylation by SGK, in the presence of a

suitable phosphate donor, of a polypeptide comprising an amino acid sequence corresponding to the consensus sequence (Arg/Lys; preferably Arg)-X-(X/Arg)-X-X-(Ser/Thr)-Z wherein X indicates any amino acid, X/Arg indicates any amino acid, with a preference for arginine, and Z

5   indicates that the amino acid residue is preferably a hydrophobic residue. The polypeptide may be Crosstide or other suitable polypeptide described in Table 1 or Table 2 or preferably a physiological substrate of SGK, which may be GSK3. It will be appreciated that SGK2 and SGK3 may be capable of autophosphorylation.   In particular, SGK2 comprises a

10   sequence corresponding to the above consensus sequence, surrounding Ser279; thus the polypeptide may be SGK2 or SGK3 or a fragment of either that comprises a potential autophosphorylation site, as discussed in Example 1, ie Ser279 of SGK2 or Ser77 or Ser 79 of SGK3.

15   It will be appreciated that in the methods of the invention wherein phosphorylation of a polypeptide may occur that the presence of a suitable phosphate donor may be required, as described for the above aspect of the invention. Suitable phosphate donors will be known to those skilled in the art and include ATP, for example as the magnesium salt (MgATP), as

20   described in Example 1.

It is preferred for at least the above three aspects of the invention that the SGK is full-length human SGK or N-terminally truncated SGK (for example, 20, 30, 40, 50 or 60 amino acids of full-length human SGK, for

25   example full-length human SGK1, may be deleted, such as in ΔN-SGK(61-431)) or a fusion (preferably a GST fusion) of full-length human SGK or N-terminally truncated SGK wherein the residue equivalent to serine 422 of full-length human SGK1 is replaced by an aspartate residue and the residues equivalent to threonine 256 and lysine 127 of the full-

length human SGK1 are unmutated, ie remain as threonine and lysine respectively.

It is preferred that the SGK is activated by phosphorylation according to a
5   method of the invention.   It will be appreciated that if the SGK is an SGK in which the residue equivalent to serine 422 of full-length human SGK1 is replaced by an aspartate residue, for example the preferred SGK described above, that this residue will not be phosphoryated, but that the SGK may be activated by phosphorylation of the residue (preferably threonine)
10 equivalent to threonine 256 of full-length human SGK1.

It will be appreciated that the SGK may be phosphorylated and/or activated in a cell by stimulating the said cell with, for example, IGF-1 or hydrogen peroxide.   The cell may be an eukaryotic, preferably
15 mammalian, for example, 293 cell in which a recombinant SGK is expressed.   The SGK may be recovered and purified as described in Example 1, for example using glutathione sepharose (for a GST-SGK fusion polypeptide), as described above and in Examples 1 and 5.

20 In an embodiment of the above methods, the compound may act by interacting with the polypeptide of the invention and modulating, ie inhibiting or enhancing, its activation by, for example, PDK1 and/or a preparation containing PDK2 activity or other activating protein kinase or protein kinases.
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It will be understood that it will be desirable to identify compounds that may modulate the activity of the polypeptide *in vivo*.   Thus it will be understood that reagents and conditions used in the method may be chosen such that the interactions between the said SGK and its activating protein

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kinase or protein kinases are substantially the same as between human SGK and its activating protein kinase or protein kinases *in vivo*, which may be PDK1 and a polypeptide with PDK2 activity. Thus, it may be preferred that the activating protein kinase used in the assay is a

5   physiological activating protein kinase of SGK, for example PDK1 or functional equivalent thereof and/or a preparation containing PDK2 activity for which interactions between the said SGK and the functional equivalent are substantially the same as between human SGK and the said physiological activating protein kinase. It will be appreciated that the

10 compound may bind to the SGK or may bind to an activating protein kinase.

By a functional equivalent of a physiological activating protein kinase of SGK, for example PDK1, is meant a protein kinase with substantially the

15 same substrate specificity as the physiological activating protein kinase, for example PDK1 (ie capable of phosphorylating the underlined residue in the consensus sequence B-T̠-F-C-G-T-(P/I)-(D/E)-Y-(L/I/M)-A-P-E, where B is a basic residue), and/or capable of phosphorylating SGK on the same residue as the said physiological activating protein kinase.

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It will be understood that it will be desirable to identify compounds that may modulate the activity of the polypeptide *in vivo*. Thus it will be understood that reagents and conditions used in the method may be chosen such that the interactions between the said SGK and its substrate are

25 substantially the same as between human SGK and its substrate or substrates *in vivo*. Thus, it may be preferred that the substrate used in the assay is a physiological substrate of SGK or a fragment, variant, derivative or fusion thereof or fusion of a said fragment, variant or derivative (defined in an analagous manner to the definitions given above

in relation to SGK) for which interactions between the said SGK and the said fragment, variant, derivative or fusion are substantially the same as between human SGK and the said physiological substrate. An example of a substrate of SGK, for example SGK1, is GSK3.

Physiological substrates of SGK may include substrates identified, for example in overexpression studies referred to in Example 1, as physiological substrates for PKB. The finding presented here concerning the activation and substrate specificity of SGK and its similarity to the activation and substrate specificity of PKB may indicate that substrates previously identified as physiological substrates for PKB may additionally or alternatively be physiological substrates for SGK, for example SGK1, SGK2 and/or SGK3.

PKB has been thought to mediate a number of the actions of insulin, including stimulation of glucose and amino acid uptake, glycogen and protein synthesis and cardiac muscle glycolysis (reviewed in [7, 8]) as well as regulation of the transcription of specific genes [9, 10]. Secondly, the PKBβ isoform is overexpressed in a significant percentage of ovarian and pancreatic cancers [11, 12] and the PKBα isoform in some breast cancers [2]. It appears that PKB or SGK may be capable of providing a survival signal that protects cells from apoptosis induced in a variety of ways (reviewed in [8, 13]). The activation of PKB or SGK by gene amplification and other mechanisms may therefore contribute to the generation of malignancies that are able to flourish in the absence of extracellular survival signals.

PKB phosphorylates proteins and peptides at serine and threonine residues that lie in Arg-Xaa-Arg,-Xaa-Xaa-Ser/Thr- sequences [14]. In insulin

42

signal transduction two physiological substrates of PKB appear to be the protein kinase -glycogen synthase kinase-3 (GSK3) [15, 16] and the cardiac isoform of phosphofructokinase-2 (PFK2) [8, 17]. Phosphorylation by PKB inhibits GSK3 activity leading to

5   dephosphorylation and activation of glycogen synthase and protein synthesis initiation factor eIF2B [18]. We show here that SGK is as effective *in vitro* at inactivating GSK3 as PKB. However, factors including the relative levels of PKB and SGK detected in appropriate tissues, suggest that PKB may be more important in the regulation of

10   GSK3 than SGK.

Dephosphorylation and activation of glycogen synthase and protein synthesis initiation factor eIF2B [18] may contribute to the insulin-induced stimulation of glycogen synthesis and protein synthesis, respectively.

15   PKB activates cardiac PFK2, which seems to underlie the insulin-induced stimulation of glycolysis in the heart. In the protection of cells against apoptosis, BAD appears to be one of the physiological substrates of PKB (and may therefore also be a physiological substrate of SGK). This protein, in its dephosphorylated form, interacts with the Bcl family

20   member Bcl$_{XL}$, thereby inducing apoptosis in some cells. However, when PKB phosphorylates BAD at Ser136, it dissociates from Bcl$_{XL}$, interacts with 14-3-3 proteins instead, and apoptosis is prevented [19]. Thus, the polypeptide BAD, which may be involved in control of apoptosis, may be a physiological substrate of SGK, for example SGK1, 2 and/or 3.

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In one embodiment, the compound decreases the activity of said SGK polypeptide. For example, the compound may bind substantially reversibly or substantially irreversibly to the active site of said polypeptide. In a further example, the compound may bind to a portion

43

of said polypeptide that is not the active site so as to interfere with the binding of the said polypeptide to its substrate. In a still further example, the compound may bind to a portion of said polypeptide so as to decrease said polypeptide's activity by an allosteric effect. This allosteric effect

5   may be an allosteric effect that is involved in the natural regulation of the said polypeptide's activity, for example in the activation of the said polypeptide by an "upstream activator" such as PDK1 and/or PDK2 (or a preparation containing PKD2 activity).

10   In a further embodiment, the compound increases the activity of said polypeptide. For example, the compound may bind to a portion of said polypeptide that is not the active site so as to aid the binding of the said polypeptide to its substrate. In a still further example, the compound may bind to a portion of said polypeptide so as to increase said polypeptide's

15   activity by an allosteric effect. This allosteric effect may be an allosteric effect that is involved in the natural regulation of the said polypeptide's activity for example in the activation of the said polypeptide by an "upstream activator" such as PDK1 and/or PDK2 (or a preparation containing PDK2 activity).

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Conveniently, the method makes use of the fact that SGK phosphorylates Crosstide as described in Example 1, but any suitable substrate, for example a physiological substrate of SGK, may be used. Thus the phosphorylation of Crosstide may be measured using techniques well

25   known to those skilled in the art.

Conveniently, the method makes use of an assay which may be substantially the same as that described in Example 1. In Example 1,

44

phosphorylation of Crosstide by SGK is measured. It is preferred that the SGK is recombinant SGK.

Alternatively, a change in the activity of the substrate may be measured. This may be done in a whole cell system or using purified or partially purified components. Thus, it will be appreciated that the phosphorylation of the substrate may be measured by measuring a change in the activity of the substrate. For example, the substrate may be GSK3 and the phosphorylation of GSK3 may be measured by measuring the activity of GSK3, as described in Example 1. It will be appreciated that it may be necessary to determine the effect of the compound on the activity of the substrate, for example by measuring the activity of the substrate when exposed to the compound (1) after exposure of the substrate to SGK, (2) before exposure of the substrate to SGK and/or (3) without exposure to SGK.

Similarly, expression of a protein encoded by an RNA transcribed from a promoter regulated (directly or indirectly) by a substrate of SGK may be measured. Expression of leptin may be affected by PKB (Barthel *et al* (1997) *Endocrinol* 183, 3559-3562) and/or SGK. The expression of the ob gene product leptin in adipose tissues has been previously described to be regulated by insulin *in vivo* and *vitro*. A constitutively active version of PKB induced production of leptin in 3T3-L1 adipocytes, possibly *via* a non-transcriptional mechanism. Leptin expression therefore may be controlled by PKB and/or SGK.

Expression of IGF-1 binding protein may be affected by PKB (Cichy *et al* (1998) *J Biol Chem* 273, 6482-6487). Expression of phosphoenolpyruvate carboxykinase (PEPCK) may also be affected by PKB (Sutherland *et al*

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(1998) *J Biol Chem* 273, 3198-3204). The protein may be one that is physiologically regulated by a substrate of SGK or may be a "reporter" protein, as well known to those skilled in the art (ie a recombinant construct may be used). A reporter protein may be one whose activity

5   may easily be assayed, for example β-galactosidase, chloramphenicol acetyltransferase or luciferase (see, for example, Tan *et al* (1996)).

A still further aspect of the invention provides a method of identifying a compound which binds to a substrate, preferably a physiological substrate,

10   of SGK, as discussed above, which may be, for example, GSK3 or BAD, and either enhances or prevents its activation and/or phosphorylation by SGK, the method comprising determining whether a compound enhances or prevents the interaction of the said substrate with SGK or determining whether the compound substantially blocks phosphorylation and/or

15   activation of the said substrate by SGK.

Suitable assays may be similar to those described above.

A further aspect of the invention is a method of identifying a compound

20   which modulates (for example, inhibits or enhances) the activation of SGK by an interacting polypeptide, preferably a physiological interacting polypeptide, as discussed above, such as PDK1 or a polypeptide with PDK2 activity (which may be present in a preparation containing PDK2 activity), the method comprising determining whether a compound

25   enhances or disrupts the interaction between (a) SGK and (b) the interacting polypeptide, such as PDK1 or a preparation containing PDK2 activity or a functional equivalent of PDK1 or PDK2, or determining whether the compound modulates (for example, enhances, or inhibits, including substantially blocks) activation of the said SGK by the

46

interacting polypeptide, such as PDK1 or a functional equivalent thereof or a preparation containing PDK2 activity or a functional equivalent thereof.

5   Expression of PDK1 is described in Example 1, in which references are also given which describe the sequence of PDK1.

A still further aspect of the invention provides a method of identifying a polypeptide that interacts with activated SGK, the method comprising (1)

10   contacting (a) the said SGK with (b) a composition that may contain a polypeptide that interacts with the said activated SGK, (2) detecting the presence of a complex containing the said SGK and a polypeptide, and optionally (3) identifying any polypeptide bound to the said protein kinase.

15   In one embodiment, the composition may comprise material from cells. In particular, the cells may be selected from the following types: (1) cells which do not express SGK even when stimulated, (2) cells which express SGK after exposure to a stimulus, but which have not been so exposed, (3) cells of type 2 after exposure to the stimulus and (4) cells of type 3 after

20   exposure to a stimulus that activates SGK (for example exposure of 293 cells to hydrogen peroxide or IGF-1). Polypeptides that are found in a subset only of types 1-4 are of particular interest and may be characterised further. Such a polypeptide may be an activator of SGK. Alternatively, it may be an inactivator of SGK.

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It will be appreciated that the method may be performed within a cell, for example using the yeast two hybrid system as is well known in the art. In this example, cDNAs copied from mRNA from the three cell types described above would be used.

It will further be appreciated that a transgenic animal in which a SGK gene is altered and/or a recombinant SGK gene is present, for example a rodent, in particular a mouse, may be useful in, for example, identifying a

5   substrate of SGK, for example a substrate of SGK1, SGK2 and/or SGK3. A said transgenic animal in which each SGK gene present is altered may be particularly useful (for example, in which at least the SGK1, SGK2 and SGK3 genes are altered). It will be appreciated that a said transgenic animal in which one or more, including all, PKB genes are also altered

10   and/or a recombinant PKB gene is present may also be useful.

Conveniently, the SGK used in a method of the invention is one which is produced by recombinant DNA technology ie is recombinant SGK. Similarly, it is preferred if the PDK1 or other "upstream activator" used

15   in the method is one which is produced by recombinant DNA technology. Similarly, it is preferred but not essential that the substrate, for example GSK3 or Crosstide, is produced by recombinant DNA technology or automated synthetic techniques, as well known to those skilled in the art. GSK3 may alternatively be purified from rabbit skeletal muscle (see

20   Example 1 and references therein).

It will be appreciated that it may be necessary to activate the SGK prior to its use in assays. In a preferred embodiment the SGK is activated *in vitro* by treating the polypeptide with PDK1 and MgATP, as described in

25   Examples 1 and 5. Recombinant or endogenous SGK may be activated in a cell, for example a 293 cell, for example by stimulation of the cell with IGF-1 or hydrogen peroxide, as described in Examples 1 and 5. It is particularly preferred if the SGK is the recombinant polypeptide produced according to the methods of the invention. It is still more preferred that

48

the SGK is SGK in which the residue equivalent to serine 422 of full-length human SGK1 is replaced by an aspartate residue and the residues equivalent to threonine 256 and lysine 127 of the full-length human SGK1 remain as threonine and lysine respectively.

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It will be appreciated that by "suitable" we mean that the said components in the method are those that have interactions or activities which are substantially the same as those of SGK or a physiological substrate of SGK or Crosstide or GSK3 or other substrates, or the upstream activator such as PDK1 as the case may be but which may be more convenient to use in an assay. For example, fusions of SGK and PDK1 are particularly useful since said fusion may contain a moiety which may allow the fusion to be purified readily.

It will be appreciated that the methods described may be performed in cells. "Reporter gene" constructs may be prepared by methods known to those skilled in the art, using the teaching herein. For example, a reporter gene construct may be made with a leptin gene promoter sequence or IGF-1 binding protein gene promoter sequence or other PKB and/or SGK-dependent promoter sequence. This construct may be introduced together with an SGK construct into a cell line, in the parent cell line of which leptin is activated in response to known stimuli, and in which the endogenous SGK gene or genes (and optionally the PKB gene or genes) have been inactivated. Alternatively the reporter gene construct could be introduced into the cell line in which SGK and a substrate of SGK is activated in response to known stimuli. The expression of the reporter gene will be dependent on the activity of SGK and thus the effect of compounds can be measured. In a further example, the reporter gene may be fatal to the cells, or alternatively may allow cells to survive under

49

otherwise fatal conditions. Cell survival can then be measured, for example using colorimetric assays for mitochondrial activity, such as reduction of WST-1 (Boehringer). WST-1 is a formosan dye that undergoes a change in absorbance on receiving electrons *via* succinate

5   dehydrogenase. In a further embodiment the yeast two-hybrid system is used.

The enhancement or disruption of the interaction between SGK and an interacting polypeptide as defined above, or suitable derivatives,

10   fragments, fusions or variants can be measured *in vitro* using methods well known in the art of biochemistry and include any methods which can be used to assess protein-protein interactions.

The said interaction can also be measured within a cell, for example using

15   the yeast two hybrid system as is well known in the art.

It will be appreciated that the invention provides screening assays for drugs which may be useful in modulating, for example either enhancing or inhibiting, the activity of SGK or its interactions with upstream activators.

20   The compounds identified in the methods may themselves be useful as a drug or they may represent lead compounds for the design and synthesis of more efficacious compounds.

It will be appreciated that screening assays which are capable of high

25   throughput operation will be particularly preferred. Examples may include the cell based assays described and protein-protein binding assays. A further example is an SPA-based (Scintillation Proximity Assay) system as described in Example 2.

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The compound may be a drug-like compound or lead compound for the development of a drug-like compound for each of the above methods of identifying a compound. It will be appreciated that the said methods may be useful as screening assays in the development of pharmaceutical

5   compounds or drugs, as well known to those skilled in the art.

The term "drug-like compound" is well known to those skilled in the art, and may include the meaning of a compound that has characteristics that may make it suitable for use in medicine, for example as the active

10   ingredient in a medicament. Thus, for example, a drug-like compound may be a molecule that may be synthesised by the techniques of organic chemistry, less preferably by techniques of molecular biology or biochemistry, and is preferably a small molecule, which may be of less than 5000 daltons and which may be water-soluble. A drug-like

15   compound may additionally exhibit features of selective interaction with a particular protein or proteins and be bioavailable and/or able to penetrate target cellular membranes, but it will be appreciated that these features are not essential.

20   The term "lead compound" is similarly well known to those skilled in the art, and may include the meaning that the compound, whilst not itself suitable for use as a drug (for example because it is only weakly potent against its intended target, non-selective in its action, unstable, poorly soluble, difficult to synthesise or has poor bioavailability) may provide a

25   starting-point for the design of other compounds that may have more desirable characteristics.

It will be appreciated that screening assays which are capable of high throughput operation will be particularly preferred. Examples may

51

include cell based assays and protein-protein binding assays. An SPA-based (Scintillation Proximity Assay; Amersham International) system may be used. For example, beads comprising scintillant and a substrate polypeptide, for example Crosstide or a peptide comprising the amino acid

5　　sequence of Crosstide may be prepared. The beads may be mixed with a sample comprising ^{32}P- or ^{33}P-γ-labelled ATP, SGK (as defined above) and with the test compound. Conveniently this is done in a 96-well format. The plate is then counted using a suitable scintillation counter, using known parameters for ^{32}P or ^{33}P SPA assays. Only ^{32}P or ^{33}P that is in

10　　proximity to the scintillant, i.e. only that bound to Crosstide that is bound to the beads, is detected. Variants of such an assay, for example in which the substrate polypeptide is immobilised on the scintillant beads *via* binding to an antibody or antibody fragment, may also be used.

15　　Other methods of detecting polypeptide/polypeptide interactions include ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Fluorescence Energy Resonance Transfer (FRET) methods, for example, well known to those skilled in the art, may be used, in which binding of two fluorescent labelled entities may

20　　be measured by measuring the interaction of the fluorescent labels when in close proximity to each other.

A further aspect of the invention is a kit of parts useful in carrying out a method, for example a screening method, of the invention. Such a kit

25　　may comprise SGK (as defined above), PDK1 or a functional equivalent thereof or a preparation containing PDK2 activity or a functional equivalent therof and/or a substrate of SGK, for example Crosstide or GSK3 or BAD.

A further aspect of the invention is a compound identifiable or identified by a method of the invention.

It is preferred that a compound of the invention does not modulate the
5   activity or activation of PKB, for example PKBα, or of PDK1. Thus, it may be desirable to assess the effect of any compound identified by a screening method of the invention on the activity or activation of PKB, for example PKBα, or PDK1. Methods of assessing the effect of any compound on the activity or activation of PKB will be known to the
10   person skilled in the art and may be similar to the methods described herein for assessing the effect of any compound on the activity or activation of SGK, with the substitution of PKB or suitable variant, fragment derivative or fusion or fusion of a suitable variant, fragment or derivative, as defined in an analagous manner to SGK, above, for SGK.

15

A further aspect of the invention is a method of identifying a substrate of SKG wherein a compound that modulates the activity of, for example inhibits, SGK but does not modulate the activity of, for example inhibit PKB, for example PKBα is used. For example, the method may be a
20   method in which the effect of a compound that inhibits SGK but does not inhibit PDK1 on cellular metabolism is assessed. Thus, for example, the effect of such a compound on signalling events thought to be mediated by activation of PKBα may be assessed, as discussed in Example 1. It will be appreciated that such a method may be carried out in whole cells or on
25   partially or semi-purified cellular components. Alternatively, a compound that modulates the activity of, for example inhibits, PKB, for example PKBα but does not modulate the activity of, for example inhibit SGK, for may be used in a method of identifying a substrate of SKG in a similar manner to that described above.

A still further aspect of the invention is a compound identifiable or identified by a method of the invention for use in medicine.

5   A further aspect of the invention is the use of a compound identifiable or identified by a method of the invention in the manufacture of a medicament for treatment of a patient in need of modulation of the activity of SGK, for example SGK1, SGK2 and/or SGK3.

10   It is preferred that the patient is mammalian. It is further preferred that the patient is human.

A compound that is capable of reducing the activity of SGK may be useful in treating cancer. PKB and/or SGK may be capable of providing a

15   survival signal that protects cells from apoptosis induced in a variety of ways (reviewed in [8, 13]). Thus, such compounds may aid apoptosis. Reduction of the activity of SGK may promote apoptosis and may therefore be useful in treating cancer. Conditions in which aiding apoptosis may be of benefit may also include resolution of inflammation.

20

It will be appreciated that a patient in need of modulation of the activity of SGK2 may have a disease or condition that affects the liver, kidney, pancreas and/or brain.

25   A compound is capable of increasing the activity of SGK may be useful in treating diabetes or obesity, or may be useful in inhibiting apoptosis. Increased activity of PKB and/or SGK may lead to increased levels of leptin, as discussed above, which may lead to weight loss; thus such compounds may lead to weight loss. For example, such compounds may

54

suppress apoptosis, which may aid cell survival during or following cell damaging processes. It is believed that such compounds are useful in treating disease in which apoptosis is involved. Examples of such diseases include, but are not limited to, mechanical (including heat) tissue injury or

5   ischaemic disease, for example stroke and myocardial infarction, neural injury and myocardial infarction. Thus the patient in need of modulation of the activity of SGK may be a patient with cancer or with diabetes, or a patient in need of inhibition of apoptosis, for example a patient suffering from tissue injury or ischaemic injury, including stroke.

10

Thus, a further aspect of the invention provides a method of treating a patient with an ischaemic disease the method comprising administering to the patient an effective amount of a compound identifiable by the screening methods of the invention.

15

A still further invention provides a use of a compound identifiable by the screening methods of the invention in the manufacture of a medicament for treating an ischaemic disease in a patient.

20   Thus, a further aspect of the invention provides a method of treating a patient with an ischaemic disease the method comprising administering to the patient an effective amount of a compound identifiable by the screening methods of the invention.

25   If the patient is a patient in need of promotion of apoptosis, for example a patient with cancer, it is preferred that the compound of the invention that is used in the preparation of the medicament is capable of reducing the activity of SGK. If the patient is a patient with diabetes or a patient in need of inhibition of apoptosis, for example a patient with ischaemic

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disease, it is preferred that the compound of the invention that is used in the preparation of the medicament is capable of increasing the activity of SGK.

5   It will be appreciated that a compound of the invention may be capable of modulating the activity of SGK1, SGK2 and/or SGK3 to different extents. It will be appreciated that it may be desirable to select a compound with a particular profile of activity against the above forms of SGK for a particular use. SGK2 mRNA is present at highest levels in liver, kidney,

10   pancreas and brain, whereas mRNA encoding SGK1 and SGK3 is similar in all tissues tested. Thus, it may be important to select a compound that is capable of increasing the activity of SGK2 for use in the preparation of a medicament for treating ischaemic liver disease.

15   The aforementioned compounds of the invention or a formulation thereof may be administered by any conventional method including oral and parenteral (e.g. subcutaneous or intramuscular) injection. The treatment may consist of a single dose or a plurality of doses over a period of time.

20   Whilst it is possible for a compound of the invention to be administered alone, it is preferable to present it as a pharmaceutical formulation, together with one or more acceptable carriers. The carrier(s) must be "acceptable" in the sense of being compatible with the compound of the invention and not deleterious to the recipients thereof. Typically, the

25   carriers will be water or saline which will be sterile and pyrogen free.

Thus, the invention also provides pharmaceutical compositions comprising the compound identifiable by the screening methods of the invention and a pharmaceutically acceptable carrier.

56

Figure Legends.

Fig. 1.

Amino acid sequences surrounding the activating phosphorylation sites on

5   PKB, p70 S6 kinase and PKCξ and their similarity to the corresponding
regions of SGK.   Identities are shown in boldface type and the
phosphorylated residues in PKB and p70 S6 kinase are underlined. The
phosphorylation sites are separated by 160-165 residues in each enzyme.

10   **Fig. 2. Expression and purification of SGK and PKB fusion proteins
in 293 cells. GST fusion proteins expressed in 293 cells were purified on
glutathione-Sepharose** from 200 µg of cell lysate protein, subjected to
electrophoresis on 5-20% (panel A) or 10% (panel B) SDS-polyacrylamide
gels and stained with Coomassie Blue. Cells were transfected with the

15   following constructs:- Lane 1, pEBG2T expressing GST; lanes 2 and 4,
PEBG-SGK expressing full length SGK; lane 3, pEBG-PKBα expressing
full length PKBα; lane 5 pEBG-ΔN-SGK(61-431) expressing the N-
terminally truncated form of SGK. The marker proteins (lanes M) and
their molecular masses are also shown.

20

**Fig. 3. Activity of GST-SGK fusion proteins purified from
unstimulated 293 cells.** Wild type SGK and the mutants indicated were
expressed in 293 cells and purified on glutathione-Sepharose. Each fusion
protein (1 µg) was incubated for 20 min at 30°C with protein phosphatase

25   2A (30 mU / ml) in 50 µl of 50 mM Tris/HCl pH 7.5, 0.1 mM EGTA, 0.
1 % (v/v) 2-mercaptoethanol. Where indicated (+), microcystin-LR (1
µM) was included prior to the addition of PP2A. In the other incubations
(-) microcystin-LR was only added after treatment with the phosphatase.
SGK activity was then measured using "Crosstide" as substrate.

Fig. 4. Phosphorylation and activation and of SGK by PDK1 *in vitro*

(A)   GST-SGK (0.3 μg) was phosphorylated using GST-PDK1 (0.1 μg)

5   and [γ-^{32}P] ATP (500 cpm / pmol) as described under Methods. Where
indicated (+), 1 μM PtdIns(3,4,5)P$_3$ in lipid vesicles containing
phosphatidylserine (100 μM) and phosphatidylcholine (100 μM) (PS/PC)
were also included. The reactions were stopped by the addition of SDS to
2% and, after heating for 5 min at 95°C, the samples were subjected to

10   electrophoresis on 10% SDS/polyacrylamide gels, stained with
Coomasssie blue and then autoradiographed.   The positions of the
molecular mass markers are also indicated (B) Same as (A), except that
unlabelled ATP was used instead of [γ-^{32}P] ATP. After incubation for 10
min at 30°C, 10 μl aliquots were assayed for SGK activity using Crosstide

15   as substrate. The results are shown ± SD for three separate experiments.

Fig.5. Effect of mutations on the phosphorylation of SGK by PDK1 *in vitro*.

(A) GST fusion proteins of wild type (WT) or mutant GSK (0.3 μg)
were incubated with PP2A as described in the legend to Fig 3 and, after

20   the addition of microcystin-LR (1 μM) to inactivate the PP2A, the SGK
proteins were incubated with [γ-^{32}P]ATP (500 cpm/pmol) with (+) and
without (-) PDK1 (0.1 μg), subjected to SDS-PAGE, stained with
Coomasssie blue and then autoradiographed. The Lys 127Ala mutation
creates a catalytically inactive mutant. (B) Same as (A), except that

25   unlabelled ATP was used instead of [γ-^{32}P] ATP (500 cpm/pmol). After
incubation for 10 min at 30 °C, 10 μl aliquots were assayed for SGK
activity using Crosstide as substrate. The results are shown ± SD for
three separate experiments. (C) GST fusion proteins of wild type SGK or
the S422D mutant (1 μg) were incubated with PP2A and phosphorylated

58

with PDK1 (0.2 μg) and [γ-^{32}P]ATP as in A, then subjected to SDS-PAGE

followed by autoradiography. (D) Same as (C), except that unlabelled

ATP was used instead of [γ-^{32}P]ATP. After incubation for 10 min at

30°C, aliquots of the reactions were assayed for SGK activity. The results

5   are shown ± SD for three separate experiments.

Fig. 6. Mapping the PDK1 phosphorylation site on SGK (A) GST-ΔN-

SGK[S422D] (26 μg) was phosphorylated with PDK1 and digested with

V8 protease as described under Methods. The digest was applied to a

10   Vydac C18 column equilibrated in 0.1 % (v/v) trifluoroacetic acid (TFA).

The column was developed with a linear gradient of acetonitrile in 0.1 %

TFA at a flow rate of 0.8 ml / min and fractions of 0.4 ml were collected.

^{32}P-radioactivity is shown by the full line and the acetonitrile gradient by

the diagonal line. The inset shows phosphoamino acid analysis of the

15   major ^{32}P_labelled peptide. (B) An aliquot of the major phosphopeptide in

panel A was analysed by solid-phase sequencing on an Applied Biosystems

470A sequencer [29] and ^{32}P-radioactivity released after each cycle of

Edman degradation was measured.

20   Fig. 7. SGK and PKBα inactivate GSK3 at similar rates.

The incubations were carried out as described for peptide phosphorylation,

except that GSK3 (50mU) purified from rabbit skeletal muscle replaced

the peptide. Units of GSK3 activity are defined in [30]. At various times

after incubation with MgATP alone (open triangles) and either SGK (open

25   circles) or PKBα (closed circles) aliquots were removed and assayed for

GSK3 activity as in [30].

Fig. 8. Activation of SGK in 293 cells.

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(A)   Cells were transiently transfected with DNA constructs expressing wild type GST-SGK (SGK-WT) or GST-SGK[T256A], then stimulated for 10 min with 50 ng /ml IGF-1 or 25 min with 2 mM hydrogen peroxide, followed by lysis in ice-cold lysis buffer. 5 µl of glutathione Sepharose

5   were added to 50 mg of cell lysate protein and after end over end rotation for 30 min at 40°C, the suspension was centrifuged for 1 min at 13,000 x g. The supernatant was discarded and the beads washed four times with 1 ml of Buffer A containing 0.5 M NaCl, then three times with Buffer B. 40 41 of 60mM Tris/HCl pH 7.5, 0.12 mM EGTA, 0. 12% (v/v) 2-

10   mercaptoethanol, 3.0 µM PKI, 1.2 µM microcystin-LR, 12 mM magnesium chloride and 36 µM "Crosstide" was added to the beads. After leaving on ice for 10 min, the beads were assayed for SGK activity at 30°C by the addition of 5 µl of 1 mM [γ-^{32}P] ATP (500 cpm/pmol). The expression of wild-type and mutants SGKs in 293 cells were similar

15   as judged by SDS/polyacrylamide gel electrophoresis followed by staining with Coomassie blue (data not shown). The results are presented $\pm$ S.D. for three separate experiments. (B) The experiment was carried with wild-type GST-SGK (SGK-WT) as in (A), except that the cells were pretreated for 10 min with 100 nM wortmannin before stimulation with IGF-1 or

20   hydrogen peroxide.

Fig. 9. Time course of activation of SGK in 293 cells.

293 cells were transiently transfected with pEBG-SGK (open circles) or pEBG-PKBα (closed circles) then stimulated with 50 ng / ml IGF-1 (A) or

25   2 mM hydrogen peroxide (B). At the times indicated, the cells were lysed and the GST-SGK or GST-PKBα purified on glutathione Sepharose as in Fig 8 and assayed. The open triangle shows the GST-SGK activity after incubation with PP2A (30 mU/ ml) as described in the legend to Fig 3. The results are presented + S.D. for a single experiment in which three

separate dishes of cells were used at each time point. Similar results were obtained in another independent experiment.

Fig. 10. Effect of mutations at Ser422 on the activation of SGK in 293 cells (A) 293 cells were transiently transfected with pEBG-SGK, pEBG-SGK[S422A] or pEBG-SGK[S422D] and then stimulated for 10 min with (+) or without (-) 50 ng/ml IGF-1. The cells were lysed and the GST-SGKs purified on glutathione-Sepharose as in Fig 8 and assayed. 50 µg of cell lysate protein was used for the assay of wild type, SGK and SGK[S422A] and 25 µg for SGK[S422D]. Each protein was expressed in similar amounts as judged from SDS polyacrylamide gel electrophoresis followed by staining with Coomassie blue (data not shown). (B, C) Same as A except that the 293 cells were transiently transfected with pEBG-SGK (B) or pEBG-ΔN-SGK (C) as indicated and stimulated for 10 min with 50 ng/ml IGF-1. 50 µg of cell lysate protein was used for the assays of wild type SGK and 10 µg for the assays of the N-terminally truncated enzyme.

Fig. 11. Nucleotide and deduced amino acid sequences of human and mouse SGK2. A, SGK2α. Residues 33-329 correspond to the kinase catalytic domain. The termination codon is marked by a solid triangle. B, SGK2β; The 5'-region of SGK2β where it differs from SGK2α. The initiating methionine which starts the sequence of SGK2α is marked by an asterisk. After this residue, the sequences of SGK2α and SGK2β are identical.

Fig. 12. Nucleotide and deduced amino acid sequences of human SGK3. Residues 93-389 correspond to the kinase catalytic domain. The termination codon is marked by a solid triangle, the three asterisks denote

the position of the most 5' ATG codon and the termination codon that immediately precedes it is underlined.

Fig. 13 Alignment of amino acid sequences of SGK isoforms.

5   The alignment of human (h) SGK1, hSGK2, murine (m) SGK2 and hSGK3 was carried out using the Clustal W program (Thompson, J.D., Higgins, D.G. and Gibson T.J. (1994) *Nuc. Acids Res.* 22,4673-4680). Identities are shaded in black and the initiation codons of SGK2α and SGK2β are indicated by arrows. The two key phosphorylation sites are

10   marked with asterisks.

Fig. 14. Expression of the mRNA encoding SGK1, SGK2 and SGK3 in different human tissues. The Northern blots containing 2 μg of poly(A)+RNA were hybridized with ^{32}P-labelled SGK1, SGK2 and

15   SGK3 cDNA probes. The membranes were then exposed to X-ray film for 3-5 days. The probe for SGK2 is common to SGK2α and SGK2β. The result obtained with a specific SGK2β probe is shown in a separate panel. The positions of standard RNA markers of defined sizes in kilobases (kb) are marked.

20

Fig. 15. Induction of the mRNA encoding SGK isoforms by different agonists.

(A) Rat2 fibroblasts that had been deprived of serum for 24h were incubated for 2h with 10% foetal bovine serum (serum) or 1 μM

25   dexamethasone (Dex) or with no further additions (control). Total RNA extracted from each dish of cells (5 μg) was subjected to electrophoresis and analysed for SGK isoform transcripts by Northern blotting. To demonstrate equivalent loading of the samples, the membranes were

reprobed with ^{32}P-labelled glyceraldehyde-3-phosphate dehydrogenase (GAPDH) DNA (bottom panel). The positions of the standard RNA markers 18S and 28S ribosomal RNA are indicated. (B) Same experiment as A using H4IIE hepatoma cells.

5

Fig 16. Expression of SGK isoforms as GST-fusion proteins in 293 cells. GST-fusion proteins were expressed in 293 cells and purified from 200 µg of cell lysate protein by chromatography on glutathione-Sepharose. Proteins eluted with 15 mM glutathione were subjected to electrophoresis on a 10 % SDS/polyacrylamide gel and stained with Coomassie Blue. Cells were transfected with following constructs: lane 1, pEBG-SGK1 expressing full-length SGK1; lane 2, pEBG-ΔN-SGK1 expressing an N-terminally truncated form of SGK1; lane 3, pEBG-SGK2β expressing full length SGK2β; lane 4, pEBG-SGK2α expressing full length of SGK2α; lane 5, pEBG-SGK3 expressing full-length SGK3; lane 6, pEBG-ΔN-SGK3 expressing an N-terminally truncated form of SGK3; lane 7, pEBG-2T expressing GST. The marker proteins (lane M) and their molecular masses are also shown.

Fig. 17. Phosphorylation and activation of wild type and mutant SGK isoforms by PDK1. A, B and C; Purified GST-fusion proteins (0.4 µg) were incubated with PP2A as described under Materials and methods, and microcystin-LR (1 µM) was then added to inactivate PP2A. The SGK isoforms (20 µg/ml) were then phosphorylated using the indicated amounts of purified GST-PDK1. After 30 min at 30°C, SGK activity was measured using Crosstide as substrate. The results are shown ± S.D. for three experiments. The closed circles show the results with wild type SGKs and the open circles results with mutant SGKs in which the residue equivalent

to Ser473 of PKB had been changed to Asp. **D, E and F;** Same as A, B

and C, except that 100 μM [γ-^{32}P] ATP (500 c.p.m / pmol) was used

instead of unlabeled ATP. The reactions were stopped after 30 min by

adding SDS and 2-mercaptoethanol to final concentrations of 1 % (w/v)

5   and 1 % (v/v), respectively, followed by heating for 5 min at 95°C,

electrophoresis on 10 % SDS/polyacrylamide gels and autoradiography.

The upper panels show results with wild type (wt) SGK isoforms and the

lower panels results with mutant SGKs. The positions of each SGK

isoform and PDK1 on the gels are marked.

10

**Fig 18. Separation of tryptic phosphopeptides from SGK2α and
SGK3 after phosphorylation by PDK1.** GST-SGK2α (upper panel) or

GST-SGK3 (lower panel) were inactivated by treatment with PP2A,

phosphorylated with PDK1 (1.5 μg/ml) and Mg[γ^{32}P]ATP (5000

15   cpm/pmol), denatured in SDS, alkylated with 4-vinylpyridine and

subjected to SDS/polyacrylamide gel electrophoresis as described in the

legend to Fig 17. The bands corresponding to SGK2α and SGK3 were

excised, eluted from the gel, precipitated with trichlroacetic acid and

digested with trypsin as decribed previously (Cuenda *et al* (1996) *EMBO J*

20   *15*, 4156-4164). The digest was applied to a Vydac C18 column

equilibrated in 0.1% trifluoroacetic acid and the ^{32}P-peptides (P) resolved

using a linear acetontirile gradient in 0.1% trifluroacetic acid at a flow

rate of 0.8 ml/min. Fractions of 0.4 ml were collected and analysed for

^{32}P-radioactivity (full line). The acetonitrile gradient is shown by the

25   diagonal broken line.

Fig. 19. Activation of SGK isoforms in 293 cells.

Cells were transiently transfected with DNA constructs expressing (A) GST-SGK1, (B), GST-SGK2α and (C) GST-SGK3. At 24 h after transfection, the cells were deprived of serum for 16 h, then exposed to 50 ng/ml IGF-1 (10 min), 400 ng/ml phorbol myristate acetate (PMA) (30

5   min), 10 % serum (30 min), 1 μM dexamethasone (Dex, 60 min), 2 mM H_2O_2 (25 min), 5 μg/ml anisomycin (AN, 30 min), 0.4 M sorbitol (30 min), hypotonic stress (1 ml of water added to 3 ml of DMEM, 30 min), UV radiation (30 min after exposure to 200 J/m2) or left untreated (control). After each treatment, the cells were lysed in ice-cold lysis

10   buffer and SGK activity in 100 μg of cell lysate protein was measured. The expression of each isoform was similar in each transfection as judged by SDS/PAGE followed by staining with Coomassie Blue (results not shown). The results are shown ± S.D. for three separate experiments.

15   **Fig. 20. Effect of PI 3-kinase inhibitors on the activation of SGK isoforms by hydrogen peroxide in 293 cells.** Cells were transiently transfected with DNA constructs expressing (A) GST-SGK1, (B) GST-SGK2α and (C) GST-SGK3. At 24 h after transfection, the cells were deprived of serum for 16 h. The transfectants were then pretreated for 10

20   min with 100 nM wortmannin or for 1 h with 100 μM LY294002 and then stimulated for 25 min with 2 mM H_2O_2. The results are shown ± S.D. for three separate experiments.

Example 1:

25   **Activation of SGK by agonists that activate phosphatidylinositide 3-kinase is mediated by PDK1 and PDK2.**

Summary. The PtdIns(3,4,5)P_3-dependent activation of protein kinase B (PKB) by 3-phosphoinositide-dependent protein kinases-1 and 2 (PDK1, PDK2) is a key event in mediating the effects of signals that activate PtdIns 3-kinase. Serum and glucocorticoid-induced protein kinase (SGK)

5   is most similar to PKB (54% identity in the catalytic domain) and, although it lacks the PtdIns(3,4,5)P_3-binding pleckstrin-homology (PH) domain, it retains the residues in PKB that are phosphorylated by PDK1 (Thr308) and PDK2 (Ser473). Here we show that, like PKB, SGK is activated via a PtdIns 3-kinase-dependent pathway when 293 cells are

10   stimulated with insulin-like growth factor-1 (IGF-1) or exposed to hydrogen peroxide. Consistent with this finding, PDK1 activates SGK in vitro by phosphorylating Thr256, the residue equivalent to Thr308 of PKB, but the rate of activation is unaffected by PtdIns(3,4,5)P_3. However, the PDK1-induced activation of SGK *in vitro* is greatly

15   potentiated by the mutation of Ser422 to Asp (the residue equivalent to Ser473 of PKB). Consistent with this finding, SGK[Ser422Asp] expressed in 293 cells is fully activated by phosphorylation even in unstimulated cells, and this activation is unaffected by inhibitors of PtdIns 3-kinase. In contrast to PKB, the mutation of Ser422 does not by itself induce any

20   activation of SGK and mutation of Thr256 to Asp abolishes activation. Our results are consistent with a model in which the activation of SGK by IGF1 or hydrogen peroxide is initiated by the PtdIns(3,4,5)P_3-dependent activation of PDK2 which phosphorylates Ser422. This is then followed by the PtdIns(3,4,5)P_3-independent phosphorylation at Thr256, catalysed

25   by PDK1, which activates SGK. Like PKB, SGK preferentially phosphorylates serine and threonine residues that lie in Arg-Xaa-Arg-Xaa-Xaa-(Ser/Thr)- motifs, and SGK and PKB inactivated glycogen synthase kinase-3 (GSK-3) at similar rates *in vitro*. These findings raise the possibility that some physiological roles ascribed to PKB based on the

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overexpression of constitutively active PKB mutants, may be mediated by SGK.

Materials and Methods

5   **Materials.** Human PDK1 was expressed as a glutathione-S-transferase (GST) fusion protein in 293 cells and purified on glutathione-Sepharose [9]. V8 protease (protease Glu-C) and complete protease inhibitor cocktail were purchased from Boehringer Mannheim. Residues 5-24 of the specific protein inhibitor of cAMP-dependent protein kinase (PKI) and all

10   other peptides were synthesised at the Department of MRC Protein Phosphorylation Unit, University of Dundee, by Mr. F.B. Caudwell. Sources of other materials are given in [6].

Buffer solutions. Buffer A was 50 mM Tris/HCl pH 7.5, 1 mM EDTA,

15   1 mM EGTA, 1 % (w/v) Triton X-100, 1 mM sodium orthovanadate, 50 mM NaF, 5 mM sodium pyrophosphate, 0.27 M sucrose, 0.1 % (v/v) 2-mercaptoethanol. Lysis buffer was Buffer A containing 1 μM microcystin-LR, plus complete protease inhibitor cocktail (one tablet / 50ml) . Buffer B was 50 mM Tris/HCI pH 7.5, 1 mM EGTA, 0.1 %

20   (v/v) 2-mercaptoethanol.

Plasmids expressing SGK and site-directed mutagenesis. A full length cDNA encoding human SGK from an infant brain library was obtained from I.M.A.G.E. Consortium (clone ID 42669) and modified by PCR

25   amplification to introduce a BamHI site at the 5' end (in frame with the GST sequence of the pEBG2T vector) and a KpnI site at the 3' end using, oligonucleotides 5'-ACA CGG ATC CGC CAC CAT GTA TCC ATA TGA TGT TCC AGA TTA TGC TAC GGT GAA AAC TGA GGC TGC TAA GGG C-3' and 5'-ACA CGG TAC CGT CGA CTC AGA GGA

AAG AGT CCG TGG GAG G-3'. The PCR product was digested with

BamHI and KpnI and inserted into the cloning site of pEBG-2T. A

truncated form of SGK (ΔN-SGK) lacking the N-terminal 60 residues was

obtained by removing the fragment between the BamHI site at the 5' of

the cDNA and a BglII site located 175bp from the initiation codon,

followed by religation after filling the gap with Klenow fragment. All of

the point mutations in the SGK gene were introduced by *in vitro*

mutagenesis using PCR.

Expression of SGK in 293 cells.

Cells were transfected with 10 μg (10 cm dish) or 3 μg (6 cm dish) of the

pEBG-SGK constructs using a modified calcium phosphate gel method [6].

At 24 h after transfection, the cells were deprived of serum for 16 h, then

incubated for 10 min with or without 100 nM wortmannin or for 1 h with

or without other inhibitors, followed by stimulation with 50 ng/ml IGF-1

or 2 mM hydrogen peroxide. The cells were lysed in 1ml of ice-cold lysis

buffer, centrifuged for 5 min at 13,000 g and GST-SGK was purified on

glutathione-Sepharose as described for PKB [6]. The glutathione-

Sepharose eluate was stored in aliquots at -80°C.

Phosphorylation and assay of SGK. Phosphorylation was carried out at

30°C in 50 μl incubations containing 50 mM Tris/HCl pH 7.5, 0.1 mM

EGTA, 0.1% (v/v) 2-mercaptoethanol, 2.5 μM PKI, 1 μM microcystin-

LR, 10 mM magnesium chloride and 100 μM ATP. Where indicated lipid

vesicles containing phosphatidylcholine (100 μM), phosphatidyl serine

(100 μM) and PtdIns(3,4,5)P$_3$ (1 μM) were also included. SGK activity

was assayed exactly as described for PKB [6] using the peptide

GRPRTSSFAEG ("Crosstide") at 30 μM as substrate. One unit of

activity (U) was that amount which catalysed the phosphorylation of 1 nmole of Crosstide in one min.

Mapping the site on SGK phosphorylated by PDK1. The N-terminally

5 truncated SGK in which Ser422 had been mutated to Asp (GST-ΔN-SGK[S422D]) (26 μg) was incubated for 20 min at 30°C with PP2A (30 mU/ml), where one unit of activity is that amount which catalyses the dephosphorylation of 1 nmole of phosphorylase *a* in one min. After addition of microcystin-LR to 1 μM to inactivate PP2A, the SGK was

10 phosphorylated by incubation for 30 min at 30°C with GST-PDK1 (2 μg) and [γ^{32}P]ATP (5,000 cpm/pmol). The reaction was stopped after 30 min by adding SDS and 2-mercaptoethanol to final concentrations of 1 % (w/v) and 1 % (v/v), respectively, followed by heating at 95°C for 5 min. The sample was then incubated for 1 h at 30°C with 2 % (v/v) 4-vinylpyridine

15 to alkylate cysteine residues, electrophoresed on a 10% SDS/polyacrylamide gel, and the ^{32}P-labelled SGK was eluted from the gel and precipitated by the addition of trichloroacetic acid to 20 % (w/v). The precipitated protein was washed six times with 0.2 ml of water, resuspended in 0.3 ml of 50 mM NH$_4$HCO$_3$ (pH 7.8), digested for 18h

20 with V8 protease (1 μg) and then chromatographed on a Vydac C18 column as described under Results. Peptide fractions were analysed on a Perceptive Biosystems (Framingham, MA) Elite STR MALDI-TOF mass spectrometer in the linear and relectron mode, using 10 mg/ml α-cyanocinnamic acid as the matrix. Phosphoamino acid analysis was

25 carried out as described in [26].

Results

Expression of SGK in 293 cells.

69

Initial attempts to express SGK with a haemaglutinnin tag at its N-terminus were unsuccessful because the expressed protein was insoluble. The work reported in this example was therefore carried out using GST-fusion proteins, which were soluble when expressed in 293 cells. Full

5   length GST-SGK (Fig 2A, lane 2) was expressed in 293 cells at a much lower level than GST-PKBα (Fig 2A, lane 3). This low level of expression appears to be due to the N-terminal 60 residues of SGK, because their removal increased the level of expression 50-250 fold (Fig 2B, lanes 4 and 5). 10-50 μg of 20% pure full length SGK and 0.5 mg of

10 80% pure ΔN-SKG(61-431) was usually obtained from 10, 10 cm diameter dishes of cells.

Phosphorylation and activation of wild type SGK by PDK1 in vitro.

The activity of GST-SGK purified from 293 cells was decreased by 70%

15 following incubation with protein phosphatase 2A (PP2A) (Fig 3), a serine/threonine-specific phosphatase, and inactivation was prevented by microcystin, a specific PP2A inhibitor [27]. Thus, the basal activity of SGK results from its phosphorylation at one or more serine/threonine residues.

20

GST-SGK could be phosphorylated by PDK1 (Fig 4A) and phosphorylation was accompanied by a 10-fold increase in the basal activity (Fig 4B). Almost the same level of activity was attained if GST-SGK was first inactivated by treatment with PP2A and then phosphorylated with PDK1

25 (data not shown). However, PDK1 phosphorylated GST-SGK much more slowly than PKBα and the maximal stoichiometry of phosphorylation that could be attained was 0.05 mol/mol, compared to 0.5 mol/mol for PKBα. Moreover, unlike the activation of PKBα, the phosphorylation (Fig 4A) and activation (Fig 4B) of SGK was unaffected by PtdIns(3,4,5)P$_3$ in the

70

presence (Fig 4) or absence (data not shown) of lipid vesicles containing phosphatidylserine and phosphatidylcholine.

Effect of mutation of Ser422 and Thr256 on the activity of SGK.

5   PKBα can be partially activated (5-fold) by mutation of Thr308 to Asp or by mutation of Ser473 to Asp, and almost fully activated (20-fold) when both mutations are combined. It was therefore of interest to study the effect of the equivalent mutations on the activity of SGK.

10   GST-SGK[T256D], GST-SGK[T256E] or GST-SGK[T256A] purified from transfected 293 cells were all much less active than wild-type SGK, the activities being similar to wild-type SGK that had been treated with PP2A (Fig 3). In contrast, GST-SGK(S422D) purified from 293 cells had a specific activity more than ten-fold higher than that of the wild-type
15   enzyme (Fig 3). However, the activity of GST-SGK(S422D) did not result from the mutation of Ser422 to Asp *per se* but from increased phosphorylation, because it could be reduced to the same level as GST-SGK[T256D] or GST-SGK[T256A] by incubation with PP2A (Fig 2).

20   GST-SGK[S422A] purified from 293 cells also had very low activity, similar to GST-SGK[T256A] or the wild-type enzyme after treatment with PP2A.

Effect of mutation of Ser422 or Thr256 on the phosphorylation of
25   **SGK by PDK1 in vitro.**

The mutation of Ser422 to Ala did not affect the extent of phosphorylation of SGK by PDK1 (Fig 5A), but reduced the extent of activation by 60% (Fig 5B). In contrast, the mutation of Thr256 to Ala (or mutation of both

71

Thr256 and Ser422 to Ala) reduced phosphorylation by 80-90% (Fig 5A) and abolished activation by PDK1 (Fig 5B).

The mutation of Ser422 to Asp stimulated the rate of phosphorylation (Fig 5C) and activation (Fig 5D) by PDK1 at least six-fold. In contrast, the GST-SGK[T256A/S422D] double mutant was not activated at all by PDK1 and phosphorylation by PDK1 was reduced by 80-90% (data not shown).

We also mutated Lys 127 in the ATP binding site to Ala to create a "kinase dead" protein. This mutant was phosphorylated at the same rate, and to the same extent, as wild type SGK (Fig 5A) and, as expected, could not be activated by PDK1 (Fig 5B).

Identification of Thr256 as the residue on SGK phosphorylated by PDK1 in vitro.

The results described above suggested that the activation of SGK by PDK1 was likely to result from the phosphorylation of Thr256. In order to investigate whether this was so, we used a form of SGK that was truncated at its N-terminus (GST-ΔN-SGK[61-431]) because this mutant was expressed at far higher levels than the wild type enzyme, and Ser422 was also mutated to Asp to to facilitate phosphorylation by PDK1. Like GST-SGK[S422D] (Fig 3), GST-ΔN-SGK(61-431)[S422D] purified from 293 cells had a high activity, which could be virtually abolished by treatment with PP2A (data not shown).

PP2A-treated GST-ΔN-SGK[S422D] was phosphorylated by PDK1 to a stoichiometry of 0.6 mol/mol protein, and the ^{32}P-labelled enzyme digested with V8 protease and chromatographed on a C18 column. One major peak and several minor peaks of ^{32}P radioactivity were observed as

72

shown in Fig 6A. Analysis of the major peak by MALDI-TOF mass spectroscopy showed that its molecular mass (1923.15) was identical to that expected for the peptide comprising residues 247-262 of SGK (NEEHNSTTSTFCGTPE) containing one phosphorylated residue.

5   Residue 247 is preceded by glutamic acid, as expected from the specificity of V8 protease. Phosphoamino acid analysis indicated that this peptide contained phosphothreonine only (inset to Fig 6A). When this phosphopeptide was subjected to solid phase sequencing, ^{32}P-radioactivity was released after the 10th cycle of Edman degradation corresponding to

10   Thr256 (Fig 6B). These results, together with those obtained using the Ser256Ala mutant (Fig 5A) indicate that SGK is phosphorylated by PDK1 at Thr256, the equivalent residue to Thr308 of PKBα.

Substrate specificity of SGK. We compared the substrate specificities of

15   SGK and PKBα towards several synthetic peptides related to "Crosstide" (Table 1). Like PKBα, SGK had an absolute requirement for an arginine residue five residues N-terminal to the site of phosphorylation since mutation, even to another basic amino acid (Lys), almost abolished activity. The presence of an Arg three residues N-terminal to the site of

20   phosphorylation was also important, but not quite as critical as for PKBα. Like PKBα, SGK required at least one residue C-terminal to the phosphorylation site and a hydrophobic residue was strongly preferred at this position, though not as critical as for PKBα. Another significant difference between PKBα and SGK was that the latter was more tolerant

25   of the substitution of serine by threonine at the site of phosphorylation. Although the results presented in Table 1 were carried out using PDK1-activated GST-ΔN- SGK[S422D], similar results were obtained with full length SGK.

73

Glycogen synthase kinase-3 (GSK-3) is a protein thought to be a physiological substrate for PKB [28]. When PKBα and SGK were matched for activity towards Crosstide, both enzymes inactivated GSK3 at similar rates (Fig 7).

5

Activation of SGK in 293 cells by extracellular signals.

PKB is activated in 293 cells in response to agonists that activate PtdIns 3-kinase, such as insulin or IGF-1 or certain adverse stimuli (heat shock, oxidative stress). Since the activation of PKB results from the

10   phosphorylation of Thr308 and Ser473, and these residues and the sequences surrounding them are highly conserved in SGK (Fig 1), we investigated whether SGK could be activated by these and/or other signals in 293 cells.

15   Cells overexpressing GST-SGK were stimulated with IGF-1 or exposed to hydrogen peroxide, which induced a 2.5-4-fold activation (Figs 8A and 8B). Activation was strongly suppressed if the cells were first pre-incubated with the PtdIns 3-kinase inhibitor wortmannin (Fig 8B). In contrast, the immunosuppressant drug rapamycin that prevents the

20   activation of p70 S6 kinase, had no effect on the activation of SGK (data not shown). SGK[T256A] could not be activated by either IGF-1 or hydrogen peroxide.

The IGF-1 and hydrogen peroxide-induced activation was caused by

25   increased phosphorylation because, like the basal activity, the stimulated activity was abolished by treatment with PP2A (Fig 9). In addition activation by these stimuli was not observed when SGK[T256A] was transfected instead of wild-type SGK (Fig 8A). The activation of

74

GSTSGK induced by IGF-1 or hydrogen peroxide was slightly slower than activation of GST-PKBα under the same conditions (Fig 9).

Phorbol myristate acetate (400 ng / ml, 30 min) or EGF (100 ng / ml, 30
5   min), which are much stronger activators of the classical mitogen-activated protein (MAP) kinase cascade in 293 cells than IGF-1, did not induce any activation of SGK (data not shown).

Activation of SGK mutants by IGF-1.

10   The activity of GST-SGK[S422D] was high in 293 cells that had not been stimulated with IGF-1 (Fig 3) and, interestingly, could not be activated further by IGF-1 (Fig 10A). Moreover, preincubation of 293 cells with 100 nM wortmannin (30 min) did not affect the high basal activity of SGK (data not shown). In contrast, GST-SGK[S422A] had very low activity in
15   293 cells that was not increased by IGF-1 (Fig 10A).

GST-ΔN-SGK was activated similarly to full-length wild-type SGK in response to IGF-1 (Figs 10B and 10C), indicating that the N-terminal non-catalytic domain is not required for activation in 293 cells.

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Discussion.

Although it is well established that SGK is the product of an immediate early gene whose levels increase within a hour in response to several agonists and pathological conditions (see Introduction), the possibility that
25   SGK is also regulated by reversible phosphorylation has not been investigated previously. In this example, we establish that the activity of SGK expressed in 293 cells is determined by its level of phosphorylation (Fig 3) which increases within minutes in response to signals that activate PtdIns 3-kinase (Figs 8 and 9). We have also provided evidence that the

75

key phosphorylation sites on SGK are Thr256 and Ser422, the residues equivalent to those on PKBα that are targeted by PDK1 and PDK2, respectively.

5   SGK is phosphorylated and activated by PDK1 *in vitro* (Fig 4) and the major site of phosphorylation is Thr256 (Fig 6). Activation is abolished, and phosphorylation greatly reduced, if Thr256 is mutated to Ala (Fig 5). Thus the PDK1-induced activation of SGK is mediated by the phosphorylation of Thr256.   However, the effects of phosphorylation
10   could not be mimicked by mutating Thr256 to an acidic residue, and such mutations actually reduced activity to the level of the PP2A-treated wild-type enzyme (Fig 3). This is similar to observations made with p70 S6 kinase [28], but is in contrast to PKBα where mutation of Thr308 to Asp causes partial activation of the enzyme [6].   The finding that
15   phosphorylation of SGK by PDK1 is not totally abolished if Thr256 is mutated to Ala (Fig 4) indicates that PDK1 is capable of phosphorylating another site(s) on GST-SGK[T256A] *in vitro*, but the identity of this site and its relevance (if any) to the activation process remains to be evaluated. The Thr308Ala mutant of PKBα (but not the wild-type enzyme) is
20   phosphorylated at Thr304 by PDK1 *in vitro* without causing any activation (results not shown).

Several lines of evidence suggest that one role for the phosphorylation of Ser422 is to accelerate phosphorylation at Thr256 by PDK1 and hence the
25   activation of SGK. Thus, GST-SGK is phosphorylated by PDK1 *in vitro* much more slowly than PKBα, but phosphorylation and activation is greatly potentiated by the mutation of Ser422 to Asp (Fig 5). The Ser422 to Asp mutation also greatly increases the activity of SGK expressed in 293 cells (Figs 3 and 9), and this results from increased phosphorylation

76

(presumably at Thr256) because it is abolished by treatment with PP2A (Fig 3) and because the Thr256Ala/Ser422Asp and Thr256Asp/Ser421-Asp double mutants are inactive.

5   If it is assumed that the Ser422Asp mutation mimics the effect of phosphorylation at this residue, and that the GST-fusion protein behaves similarly to wild-type SGK, then the following model for the activation of SGK would be consistent with the results obtained in this paper. (1) The PtdIns(3,4,5)P$_3$ generated in response to IGF-1 or hydrogen peroxide

10   activates PDK2 (or a closely related enzyme), which then phosphorylates SGK at Ser422. (2) The phosphorylation of Ser422 greatly potentiates the rate at which SGK is phosphorylated and activated by PDK1 (or a closely related enzyme). This model explains why the IGF-1 induced or hydrogen-peroxide induced activation of SGK in 293 cells is suppressed

15   by wortmannin (Fig 8B), why the activation of SGK by PDK1 *in vitro* is independent of PtdIns(3,4,5)P3 (Fig 4) and why the activity of GST-SGK[S422D] is not suppressed by wortmannin. This model is similar to the mechanism proposed for the activation of p70 S6 kinase [15, 16] but, in order to validate it, it will be necessary to find out whether PDK2 is

20   indeed PtdIns(3,4,5)P$_3$-dependent, and to study the effect of PDK2 on the activation of SGK in the presence and absence of PDK1.

The mechanism of activation of SGK differs from that of PKB in several respects. Firstly, the binding of PtdIns(3,4,5)P$_3$ to the PH domain of PKB

25   is essential before any activation can take place [7]. Secondly, the interaction of PtdIns(3,4,5)P$_3$ with the PH domain of PKB causes its recruitment to the plasma membrane, which may facilitate its activation by menbrane associated PDK1 and PDK2. Thirdly, PDK1 greatly facilitates the PtdIns(3,4,5)P$_3$-dependent activation of PKB in lipid vesicles *in vitro*,

77

and may therefore also be critical for the activation of PKB at the plasma membrane *in vivo*. These differences may explain why essentially no activation of PKB occurs *in vivo* until PtdIns(3,4,5)P₃ is elevated and the larger and more rapid activation of PKB by IGF-1 or hydrogen peroxide

5   in 293 cells (Fig 9). However, like the activation of SGK, the activation of PKB may also be dependent on the interaction of PtdIns(3,4,5)P₃ with PDK2.

Like PKB and p70 S6 kinase, SGK phosphorylates peptides at serine or

10   threonine residues that lie in sequences with arginine residues at positions n-3 and n-5 and a large hydrophobic residue at position n+1, where n is the site of phosphorylation. The physiological substrates of SGK are unknown. However, like PKB, SGK is activated by a PtdIns 3-kinase dependent pathway and (unlike p70 S6 kinase) activation is not prevented

15   by the immunosuppressant drug rapamycin. Moreover, when matched for activtiy towards the standard peptide substrate Crosstide, SGK and PKBα catalysed the inactivation of GSK3 at similar rates (Fig 7). Since GSK3 is thought to be a physiological substrate of PKB [30], it is therefore possible that some of the physiological roles ascribed to PKB based on the

20   overexpression of constitutively active mutants (reviewed in [2]), may actually be mediated by SGK. Since PKB and SGK may well be activated by the same protein kinases in vivo (PDK1 and PDK2), it may not be possible to distinguish their physiological roles by the use of dominant negative mutants. The developments of drugs that inhibit PKB but not

25   SGK, and *vice versa*, or the generation of mouse "knockouts" may be necessary to answer these questions.

78

Table 1: Comparison of the activity of SGK and PKBα towards synthetic peptides related to Crosstide.

The experiments were carried out with GST-ΔN-SGK and GST-PKBα purified from 293 cells and activated by PDK1. The activities are presented relative to peptide 1 (Crosstide). The concentration of each peptide was 30 µM. Amino acid substitutions are underlined. The serine residue in Crosstide that is phosphorylated by PKB is marked with an asterisk.

	Peptide	SGK	PKBα
	*		
1	GRPRTSSFAEG	100 %	100 %
2	RPRTSSF	154	160
3	RPRTSAF	<1	<1
4	PRTSSF	<1	<1
5	RPRTSS	10	<1
6	RPRTSTF	156	208
7	RPRAATF	73	55
8	KPRTSSF	2	6
9	RPKTSSF	49	26
10	RPRTSSF	154	160
11	RPRTSSL	135	69
12	RPRTSSV	131	67
13	RPRTSSA	107	26
14	RPRTSSK	146	48
15	RPRTSSE	84	21

Example 2: Alternative assays

79

A Scintillation Proximity Assay (SPA) system (Amersham International) is used to assess the incorporation of ^{32}P radioactivity into Crosstide. In this system, the sample (containing GST-ΔN-SGK activated by PDK1 or GST-ΔN-SGK[Ser422Asp] activated by PDK1, the compound to be tested and

5   [γ-^{32}P]ATP or [γ-^{33}P]ATP is mixed with beads comprising scintillant and antibodies that bind Crosstide. Conveniently this is done in a 96-well format. The plate is then counted using a suitable scintillation counter, using known parameters for ^{32}P or ^{33}P SPA assays. Only ^{32}P or ^{33}P that is in proximity to the scintillant, i.e. only that bound to Crosstide that is then

10   bound by the antibody, is detected.

Example 3: Assay for compounds which modulate SGK activity

An assay is set up with Crosstide, as described in Example 1 or Example 2. Compounds are tested in the assay and those that give rise to inhibition

15   or activation of SGK are selected for further study. Compounds are further tested for effects on PKBα and those that do not affect the phosphorylation of Crosstide by PKBα are selected.

The compounds tested may be compounds selected on the basis of known

20   properties, for example ability to inhibit other protein kinases, such as PKBα, or may be part of a library of compounds assembled for testing in a variety of screens, for example in a "lead generation" screening programme. The compounds may be natural or synthetic, and may be generated by combinatorial chemistry, as known to those skilled in the art.

25

The selected compounds may be used in the design of further compounds for manufacture and test, in order to develop a structure-activity relationship (SAR).

Example 4: Assay for polypeptides that interact with SGK

A yeast two hybrid assay system is set up to identify polynucleotides encoding polypeptides that are capable of associating with SGK in a stable enough manner to allow transcriptional activation to occur. The polynucleotides are (in separate experiments) cDNAs copied from mRNA from cells that are capable of expressing SGK, before or after stimulation capable of stimulating expression of SGK, before or after further stimulation capable of activating the expressed SGK, and from cells which do not express SGK. Interactions which are found in a subset only of these cell types are of particular interest.

The polypeptide encoded by the polynucleotide is determined by sequencing the insert by the Sanger method as described in Example 1 and well known to those skilled in the art to obtain a predicted amino acid sequence.

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Example 5: Characterisation of the structure and regulation of two novel isoforms of serum and glucocorticoid-induced protein kinase.

Abbreviations:- SGK, serum and glucocorticoid-regulated protein kinase; PKB, protein kinase B, PDK1, 3-phosphoinositide-dependent protein

kinase-1; protein kinase C-related protein kinase-2 (PRK2); PI, phosphatidylinositol; IGF1, insulin-like growth factor-1; GSK3, glycogen synthase kinase-3; GST, glutathione S-transferase; PMA, phorbol myristate acetate; PP2A, protein phosphatase 2A; PCR, polymerase chain

5   reaction.

We show in Example 1 and [18] and subsequently others [19] have shown that, like PKB, SGK is also activated within minutes *via* a phosphorylation mechanism when cells are stimulated with insulin, insulin-like growth

10   factor-1 (IGF1) or serum, or exposed to oxidative stress.

Here, we identify two novel isoforms of SGK, termed SGK2 and SGK3, which are the products of distinct genes, and compare their tissue distribution, induction by serum and glucocorticoids, activation by

15   phosphorylation and substrate specificity with SGK (hereafter termed SGK1). Despite, their high degree of sequence similarity with SGK1, the mechanisms that regulate the level and activity of SGK2 and SGK3 differ significantly from SGK1 in several respects.

20   Like SGK1, the mRNA encoding SGK3 is expressed in all tissues examined, but SGK2 mRNA is only present at significant levels in liver, kidney and pancreas and, at lower levels, in the brain. The levels of SGK2 mRNA in H4IIE cells and SGK3 mRNA in Rat2 fibroblasts are not increased by stimulation with serum or dexamethasone, whereas the level

25   of SGK1 mRNA is increased greatly by one or both agonists. SGK2 and SGK3 are activated *in vitro* by PDK1, albeit more slowly than SGK1, and their activation is accompanied by the phosphorylation of Thr193 and Thr253, respectively, the residues equivalent to the Thr in the "activation

loop" of PKB that is targetted by PDK1.   The PDK1-catalysed phosphorylation and activation of SGK2 and SGK3, like SGK1, is greatly potentiated by mutating Ser356 and Ser419, respectively, to Asp, these residues being equivalent to the C-terminal phosphorylation site of PKB.

5   Like SGK1, SGK2 and SGK3 are activated five-fold via a phosphorylation mechanism when cells are exposed to hydrogen peroxide but, in contrast to SGK1, activation is only suppressed partially by inhibitors of PI 3-kinase.   SGK2 and SGK3 are activated to a smaller extent by IGF1 (2-fold) than SGK1 (5-fold).   Like PKB and SGK1, SGK2 and SGK3

10   preferentially phosphorylate Ser and Thr residues that lie in Arg-Xaa-Arg-Xaa-Xaa-Ser/Thr motifs.   This raises the possibility that some physiological roles ascribed to PKB on the basis of overexpression studies with constitutively active mutant enzyme, may be mediated by isoforms of SGK.

15

Materials and methods

Materials. Human PDK1 was expressed as a glutathione S-transferase (GST) fusion protein in 293 cells and purified by affinity chromatography on glutathione-Sepharose [5].   Dexamethasone, wortmannin and LY

20   294002 were purchased from Sigma (Poole, U.K.).   All peptides were synthesized by Dr Graham Blumberg (Department of Biochemistry, University of Bristol, U.K.). Expression plasmids of SGK1 and an N-terminally truncated form of SGK1 ΔN-SGK1[61-431]) were identical to pEBG-SGK and pEBG-ΔN-SGK[61-431] described in Example 1 and [18].

25   The pEBG-2T-2 vector was made by insertion with 5'-GAT CTC GGA TCC ACT AAC GGT AC-3' and 5'-CGT TAG TGG ATC CGA-3' between BamHI and KpnI sites of pEBG-2T.   This introduced a new

84

BamHI site which was located in a different reading frame from the original pEBG-2T vector.

Buffer solutions. Buffer A comprised 50 mM Tris/HCl, pH 7.5, 1 mM EDTA, 1 mM EGTA, 1% (w/v) Triton X-100, 1 mM sodium orthovanadate, 50 mM NaF, 5 mM sodium pyrophosphate, 0.27 M sucrose, and 0.1 % (v/v) 2-mercaptoethanol. Buffer B comprised 50 mM Tris/HCl, pH 7.5, 1 mM EGTA, 0.1 % (v/v) 2-mercaptoethanol. Buffer C comprised 50 mM Tris/HCl, pH 7.5, 150 mM NaCl, 0.1 mM EGTA , 0.5 mM dithiothreitol and 1 mg/ml bovine serum albumin. Cell lysis buffer was Buffer A containing 1 μM microcystin-LR, 0.2 mM phenylmethylsulphonyl fluoride and protease-inhibitor cocktail (one tablet / 500 ml). .

Cloning of SGK isoforms. A full length clone encoding human SGK2 was obtained as follows. Analysis of expressed sequence tag (EST) AA130828 (IMAGE Consortium, St. Louis, MO, USA) showed that it encoded a novel kinase which was homologous to human SGK1. A 5' - RACE was then carried out using human kidney cDNA (Marathon-Ready cDNA, Clontech, CA, USA) as a template, since there was no stop codon upstream of first ATG. The primers used for 5'-RACE of SGK2 were 5'- GCT CTG GAC TTG GGG TCC CAG CTG GGC-3', 5'-GTT GAT GTT CCC ATT GGC CCT GGA GGG-3' and 5'-GCT GGG CAT TTG GGT TGG CTG AAG GCC-3'. Fragments of 200-220 bp were obtained in all three cases and the PCR products were cloned into the pCR-2.1-TOPO vector (Invitrogen, USA). Eight clones out of 10 clones analysed possessed a 200 bp fragment and sequence analysis showed that these corresponded to the 5' portion of EST AA130828. We designated this protein kinase as SGK2α. Two other clones had longer fragments (500 and 600 bp). Sequence analysis showed that these clones corresponded to

85

another form of SGK2 with an additional 60 amino acid residues at the N-terminus and a different 5' non-coding region. This enzyme was designated SGK2β. A mouse clone (accession number AI 386362) was also identified by interrogating the NCBI EST database with the sequence

5   of human SGK2α, that was predicted to encode a full length protein of mouse SGK2α. We also assembled the full length murine cDNA using the clones AA790370 (which encodes the first 1240 nucleotides) and AA138663 (that starts from nucleotide 1140 and terminates in the polyA tail).

10

A full length clone encoding human SGK3 was obtained as follows. Analysis of EST AA219166 (IMAGE Consortium) showed that it encoded the partial sequence of a novel protein kinase which had homology to SGK1 and SGK2. Since this cDNA contained a gap in the central portion,

15   a PCR reaction was carried out using a human skeletal muscle library as a template.   The   Primers   used   for   the   PCR   were   5'-AACATCCGTTTTTGGTTGGATTGC-3'   and   5'-GGGTAGATGTTAGTGTAAAC-3'. Since this clone did not contain an initiating ATG codon, 5'-RACE was carried out using human kidney

20   cDNA as a template. The primers used for 5'-RACE were 5'-ATA AAG TTC TGG ATA CCT AAC TAG G-3', 5'-GAA GGA ATG CTC TGA CAT CTG GAT GG-3' and 5'-GAT CTG ACT GGT GTT TTG GAC TGT CC-3'). Unlike the 5' RACE of SGK2, which showed sharp bands of PCR products when analysed on an agarose gel, that of SGK3 produced

25   a smear. We therefore ligated these heterogeneous products into a pCR-2.1-TOPO vector (Invitrogen, USA) and analyzed the 20 clones obtained. Sequence analysis revealed that 12 clones contained the missing part of the new SGK sequence, which we called SGK3.

In order to introduce a BamHI site at the 5'-end in-frame with the GST

sequence of the pEBG-2T-2 vector, and a NotI site at the 3'-end of each

open reading frame, PCR amplification was performed using the following

5   primers: SGK2α: 5'-GGA TCC AGC TGC CTG ATC ATT GCT AC-3'

and 5-GCG GCC GCC TAG CAA TCC AAG ATG TCA TC-3; SGK2β:

5'-GGA TCC CAG GGG TTG CTT ACC TCG GG-3'and 5'-GCG GCC

GCC TAG CAA TCC AAG ATG TCA TC-3' ; full length SGK3 : 5'-

GGA TCC AAG CCC TGA AGA AGA TTC CTG CC-3' and 5'-GCG

10   GCC GCT CAC AAA AAT AAG TCT TC-3' ; SGK3 lacking the N-

terminal 52 residues (ΔN-SGK3[53-429]) : 5'-GGA TCC TGG ACA GTC

CAA AAC ACC AG-3' and 5'-GCG GCC GCT CAC AAA AAT AAG

TCT TC-3'. The PCR products were cloned into a pCR-2.1-TOPO vector

(Invitrogen) and sequenced. Each fragment was digested with BamHI and

15   NotI and inserted into the cloning site of pEBG-2T-2. Ser356 of

SGK2α and Ser419 of SGK3 were mutated to Asp by in vitro mutagenesis

using PCR.

Expression of SGK isoforms in 293 cells. Each 6cm and 10 cm diameter

20   dish of cells were transfected with 10 μg or 3 μg, respectively, of the

pEBG-SGK constructs using a modified calcium-phosphate method [3]. At

24 h after transfection, the cells were deprived of serum for 16 h, then

stimulated in one of the following ways: 50 ng/ml IGF-1 (10 min), 400

ng/ml phorbolmyristate acetate (PMA) (30 min), 10 % foetal bovine

25   serum (30 min), 1 μM dexamethasone (60 min), 2 mM H_2O_2 (25 min), 5

μg/ml anisomycin (30 min), 0.4 M sorbitol (30 min), 30 min of hypo-

osmotic stress (3 ml of DMEM diluted to 4 ml with water) and UV-C

irradiation (200 J/m²). After each treatment, the cells were lysed and the

activity of SGK isoforms was measured after affinity purification of the GST-fusion proteins on glutathione Sepharose, as described previously for SGK1 [18].

5   **Dephosphorylation, phosphorylation and assay of SGK isoforms *in vitro*.**

Each GST-SGK isoform (0.4 µg) was incubated for 20 min at 30°C with protein phosphatase 2A (PP2A, 30 mU/ml) in a 10 µl incubation containing 20 mM Tris/HCl, pH 7.5, 0.1 % (v/v) 2-mercaptoethanol, 0.1

10   mM EGTA and 1 mg/ml bovine serum albumin. After addition of microcystin-LR to 1 µM to inactivate PP2A, SGK (0.4 µg) was phosphorylated for 30 min at 30°C in a mixture (20 µl) containing 50 mM Tris/HCl, pH 7.5, 10 mM MgCl2, 0.1 % (v/v) 2-mercaptoethanol, 0.1 mM EGTA, GST-PDK1 (0.03-300 ng) diluted in Buffer C and 100 µM

15   unlabelled ATP. SGK assays were initiated by the addition of 30 µl of a mixture containing 50 mM Tris/HCl, pH 7.5, 10 mM $MgCl_2$, 0.1 % (v/v) 2-mercaptoethanol, 0.1 mM EGTA, 100 µM [γ-^{32}P] ATP (500 c.p.m / pmol), 50 µM of the peptide substrate Crosstide (GRPRTSSFAEG) and 4.2 µM of residues 5-24 of the specific protein inhibitor of adenosine 3'5'

20   cyclic monophosphate-dependent protein kinase. After 10 min at 30°C, the reactions were terminated by spotting aliquots on to P81 phosphocellulose paper, followed by immediate immersion in 75 mM phosphoric acid. The papers were washed, dried and analysed [3]. One unit (U) of SGK was that amount which phosphorylated 1 nmole of

25   Crosstide in one min.

Preparation of RNA and Northern blotting. Rat2 fibroblasts or H4IIE hepatoma cells (10^6 cells) were plated on to 10 cm dishes and incubated for 24 h in Dulbecco's modified Eagles' medium (DMEM) containing 10

88

% foetal bovine serum (FBS). The medium was changed to DMEM without serum and the cells incubated for a further 24 h. After stimulation with 10% FBS and 1 µM dexamethasone, total RNA was isolated from the cells using an RNeasy Mini kit (QIAGEN,West Sussex, UK). RNA (5 µg)

5 was electrophoresed through 1.2 % agarose gels in presence of 0.67 M formaldehyde, transferred to Hybond-N+ (Amersham Pharmacia Biotech, UK) and cross-linked under ultraviolet light (UV Stratalinker, Stratagene, La Jolla, CA, USA). ^{32}P-labelled probes were generated by labelling the open reading frames of each SGK isoform with [γ-^{32}P] dATP using a

10 Multiprime DNA labelling kit (Amersham Pharmacia Biotech). Hybridization was performed in Rapid-hyb buffer (Amersham Pharmacia Biotech) for 2 h at 65°C. Membranes were washed with 2 x SSC/0.1 % SDS for 30 min at room temperature and then for 15 min at 65°C, then washed with 0.2 x SSC/0.1 % SDS for 15 min at 65°C and exposed to X-

15 ray film (Hyperfilm, Amersham) at -70°C for 3-5 days.

Results.

Cloning of novel SGK isoforms. SGK was originally identified as a glucocorticoid and osmotic stress-responsive gene (see Introduction).

20 Searching for new SGK isoforms, the NCBI database was interrogated with the sequence of SGK. This search identified two human ESTs that showed considerable similarity to the original gene. Sequence analysis of these ESTs revealed that they represent two new isoforms of the SGK gene family, that we term SGK2 and SGK3. The original SGK isoform is

25 therefore termed SGK1.
As none of these ESTs were full length clones, 5' RACE and PCR reactions were carried out to obtain the missing parts of the sequence (see Methods). This led to the identification of two splice variants of SGK2,

termed SGK2α and SGK2β (Fig 11). SGK2α encodes a protein of 368 residues with a calculated molecular mass of 41.1 kDa, SGK2β a protein of 428 amino acids with a calculated molecular mass of 47.6 kDa. An EST encoding murine SGK2α was also identified (Fig 13). Unlike

5   human SGK2α, the murine cDNA contains an in-frame stop codon immediately preceding the initiating Met. This establishes that the shortest splice variant does indeed start at this position.

The nucleotide sequence of SGK3 contained two in frame ATG codons

10   (Fig 12). The sequence surrounding the second ATG conforms more closely to the consensus that frequently surrounds initiation codons. Moreover, a stop codon (TAA) is present immediately upstream of the first ATG (Fig 12). For these reasons, the site of initiation is assumed to be the second ATG. This would encode a 430 residue 49.0 kDa protein.

15   If the first ATG is used for initiation, it would generate a polypeptide 62 amino acids longer.

The amino acid sequences of the three SGK isoforms are about 80 % identical to one another in the catalytic domain, while the short C-

20   terminal non-catalytic domains are less similar (44-68 % identity). The N-terminal 85 residues that precede the catalytic domain are much less similar. In this region there is only about 25% identity between SGK1 and SGK3 and almost no identity between SGK2 and the other isoforms (Fig 13).

25   **Tissue distribution of SGK isoform mRNAs.** As reported previously by others [13], the level of SGK1 mRNA was similar in all tissues tested, with a major 2.6 kb transcript and a minor 7 kb transcript. The highest levels of both transcripts were in the pancreas. The level of SGK3 mRNA

was also similar in each tissue, with a major 5 kb transcript in each case.
In contrast, mRNA which hybridises with a probe that recognises SGK2α
and SGK2β had a much more restricted tissue distribution, 2.1 kb and 4.0
kb transcripts being present in liver, kidney, pancreas and brain (Fig 14).

5   An SGK2β-specific probe also recognised transcripts in liver and kidney,
but the levels were much lower and the signal was rather diffuse.

**Effect of serum and dexamethasone on the level of SGK isoform
mRNA in Rat2 fibroblasts and H4IIE hepatoma cells.** SGK1 is an

10   immediate early gene and its mRNA increases greatly within one hour of
stimulation with serum and glucocorticoids in several cell lines [11]. We
therefore examined the effects of these stimuli on mRNA encoding all
three SGK isoforms. In Rat2 fibroblasts SGK1 mRNA was strongly
induced by serum or dexamethasone after 2 h as expected, whereas the

15   level of SGK3 mRNA was not affected by these agonists. SGK2 mRNA
was not expressed in Rat2 fibroblasts (Fig 15A). In rat H4IIE hepatoma
cells dexamethasone, but not serum, induced the formation of SGK1
mRNA, whereas the level of SGK2 mRNA was unaffected by either
agonist. SGK3 mRNA was not expressed in H4IIE cells (Fig 15B)

20

Expression of SGK isoforms in 293 cells. All three isoforms were
expressed as GST-fusion proteins in 293 cells. The sizes of GST-
SGK2α (70 kDa), GST-SGK3 (75 kDa) and GST-ΔN-SGK3 (70 kDa)
were consistent with their calculated molecular masses (Fig 16).

25   However, nearly all the GST-SGK2β was expressed as free GST (25 kDa)
presumably due to proteolysis of the full length fusion protein (Fig 16,
lane 3). Deletion of the N-terminal region of SGK3 improved its level of
expression (Fig 16, lanes 5 and 6), although not to the same extent as

SGK1 (Fig 16, lanes 1 and 2). Typically 400 μg, 100 μg and 150 μg of 90 % pure GST-ΔN-SGK1[61-431], 80 % pure GST-SGK2α and 90 % pure GST-ΔN-SGK3[53-429], respectively, were obtained from ten, 10 cm diameter dishes of cells.

5

Phosphorylation and activation of SGK isoforms by PDK1. The two key phosphorylation sites corresponding to residues Thr308 and Ser473 of PKBα [3] are conserved in SGK2 (Thr193 and Ser356 in SGK2α) and SGK3 (Thr253 and Ser419), as well as SGK1 (Thr256 and Ser422). We

10   (Example 1 and [18]) and subsequently others [19] have shown that PDK1 activates wild type SGK1 *in vitro* by phosphorylating Thr256 (see also Fig 17A and 17D). Wild type SGK2α and SGK3 were also activated by PDK1 *in vitro*, although higher concentrations of PDK1 were required for activation (Figs 17B and 17C) and phosphorylation (Figs 17E and 17F),

15   especially with SGK2. Maximal activation of all SGK isoforms was observed after incubation for 30 min with 1.5 μg/ml PDK1 (Figs 17A, 17B and 17C). At this concentration of PDK1, the stoichiometries of phosphorylation were close to 1 mol / mol for SGK1 and SGK3 and 0.2 mol/mol for SGK2 (data not shown). If the PDK1 concentration was

20   increased 10-fold, the level of phosphorylation of SGK2 and SGK3 increased considerably, but without any further activation (Figs 17D, 17E and 17F). This suggested that PDK1 is capable of phosphorylating other sites on SGK2 and SGK3 that do not affect activity directly.

We have demonstrated that an SGK1 mutant in which Ser422 (the PDK2

25   site) is mutated to aspartic acid has a specific activity more than 10-fold higher than that of the wild type enzyme after expression in 293 cells (Example 1 and [18]). This high basal activity results from increased phosphorylation at Thr256, and can be abolished by treatment with PP2A

(Example 1 and [18]). In the present study, we found that PP2A-treated SGK1 [Ser422Asp] was reactivated (Fig 17A) and phosphorylated (Fig 17D) at a much higher rate than PP2A-treated wild type SGK1.

5   The corresponding mutants of SGK2 and SGK3 in which the serines equivalent to Ser422 of SGK1 were mutated to aspartic acid (SGK2[Ser356Asp] and SGK3[Ser419Asp]) also had high activities after expression in 293 cells (data not shown). After treatment with PP2A, SGK2α was inactivated and, as for SGK1, SGK2[Ser356Asp] was

10   activated (Fig 17B) and phosphorylated (Fig 17E) by PDK1 much more effectively than wild type SGK2α. In contrast SGK3[Ser419Asp] could not be inactivated by PP2A and incubation with PDK1 and MgATP did not increase activity further (Fig 17C). SGK3[Ser419Asp] did however become phosphorylated upon incubation with MgATP even in the absence

15   of PDK1 (Fig 17F), presumably as a result of autophosphorylation. Phosphorylation did not appear to be catalysed by PDK1 present as a contaminant, because no PDK1 could be detected in the preparation by immunoblotting (data not shown).

20   The SGK2[Ser356Asp] mutant and wild type SGK3 were incubated for 30 min at 30°C using 1.5 μg/ml PDK1 and MgATP which led to the incorporation of 1.2 and 1.3 mol phosphate per mol protein, respectively. The reactions were terminated, digested with trypsin and phosphopeptides chromatographed on a C18 column as in Example 1 and [18] (Fig 18).

25   The major phosphothreonine-containing peptides from the SGK2 and SGK3 digests (peptides P2 and P5 in Figs 18A and 18B) were subdigested with N-Asp proteinase and subjected to MALDI-TOF mass spectrometry and solid phase Edman sequencing [20] to identify the sites of

phosphorylation. These experiments revealed that the phosphopeptide from SGK2 corresponded to residues 189-207 phosphorylated at Thr193, while the SGK3 phosphopeptide corresponded to residues 249-267 phosphorylated at Thr253. These experiments establish that PDK1 does

5   indeed phosphorylate SGK2 and SGK3 at sites equivalent to Thr256 of SGK1.

The phosphoserine-containing tryptic peptides P1, P3 and P4 (Fig 18) were also analysed by MALDI-TOF mass spectrometry and Edman

10   sequencing. These experiments revealed that peptide P1 corresponded to residues 277-287 phosphorylated at Ser279, while peptide P3 comprised residues 334-367 phosphorylated at Ser334. Peptide P4 corresponded to residues 73 to 99 and was phosphorylated at either Ser75 or Ser77; the latter was the major site of phosphorylation. These findings are

15   considered further under discussion.

The activation of SGK2 and SGK3 by PDK1 was unaffected by lipid vesicles containing phosphatidylserine and phosphatidylcholine, and slightly inhibited by the further inclusion of 10 μM PI 3,4,5-trisphosphate

20   (data not shown). These results are similar to those obtained previously with SGK1.

Substrate specificities of SGK isoforms. We have shown that SGK1 and PKB have similar specificities towards a panel of synthetic peptides,

25   preferentially phosphorylating serine and threonine residues that lie in Arg-Xaa-Arg -Xaa-Xaa-Ser/Thr motifs (Example 1 and [18]). In the present Example, the specificity requirements of SGK2α and SGK3 were also found be similar (Table 2), although SGK3 appears to tolerate the

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presence of a lysine instead of an arginine at position n-3 (when n is the site of phosphorylation) a little better than SGK1 or SGK2α (Table 2).

Table 2. Comparison of the activity of SGK isoforms toward synthetic
5   **peptides related to Crosstide.**

The experiments were carried out with GST-ΔN-SGK1[S422D], GST-SGK2α[S356D] and GST-ΔN-SGK3[S419D] purified from 293 cells. The activities are presented relative to peptide 1 (Crosstide). The concentration of each peptide was 30 μM. Amino acid substitutions to peptide 2 are
10   underlined. The result shown is the average of two experiments each agreeing to ±10 %.

	Peptide	SGK1 activity %	SGK2 activity %	SGK3 activity %
1	GRPRTSSFAEG	100	100	100
2	RPRTSSF	135	182	137
3	RPRTSAF	<1	<1	<1
4	PRTSSF	<1	<1	<1
5	RPRTSS	5.1	8	18
6	RPRTSTF	129	192	156
7	RPRAATF	44	61	56
8	KPRTSSF	<1	<1	<1
9	RPKTSSF	11	8	48
10	RPRTSSF	135	182	137
11	RPRTSSL	108	185	113
12	RPRTSSV	90	124	139

13	RPRTSS<u>A</u>	49	82	123
14	RPRTSS<u>K</u>	84	128	200
15	RPRTSS<u>E</u>	28	34	67

Activation of SGK isoforms in 293 cells.   Each SGK isoform was expressed in 293 cells and their ability to be activated acutely by a variety of stimuli was examined.   As reported previously (Example 1 and [18, 19]), stimulation with IGF1 induced a four to five-fold increase in SGK1 activity (Fig 19), which reached a maximum after 10 min (data not shown).   In contrast, SGK2α and SGK3 were only activated two-fold by IGF1 (Fig 19).   Activation was maximal after 5 min and sustained for at least 20 min (data not shown).   The agonist which produced the strongest activation of SGK2α and SGK3 (5-fold) was hydrogen peroxide similar to that observed with SGK1 (Fig 19).   Serum was also a weak activator of all three isoforms.   However, osmotic shock (treatment with 0.4M sorbitol), which potently inhibited SGK1, had no effect on the activity of SGK2α or SGK3 (Fig 19).

The activation of SGK2 and SGK3 induced by hydrogen peroxide was only inhibited partially when the cells were preincubated with wortmannin or LY 294002 (two inhibitors of PI 3-kinase) prior to stimulation with hydrogen peroxide.   In contrast, the activation of SGK1 was abolished (Fig 20).

Discussion.   In this Example we identify two novel isoforms of SGK1, termed SGK2 and SGK3, which share 80% identity with SGK1 in their catalytic domains.   Nevertheless, despite this similarity, SGK2 and SGK3 differ significantly from each other, and from SGK1, in a number of

respects. Firstly, the mRNAs encoding SGK1 and SGK3 are widely expressed, but that encoding SGK2 has a more restricted distribution, being highly expressed in liver, kidney and pancreas and, at lower levels, in the brain (Fig 4). Secondly, SGK2 mRNA and SGK3 mRNA are not

5 increased by cell stimulation with serum or glucocorticoids (Fig 15), whereas SGK1 mRNA levels increase greatly within 1h of exposure to these agonists ([11], Fig 15).

SGK2 and SGK3 are activated by PDK1 in vitro, albeit more slowly than

10 SGK1 (Fig 17), and activation is accompanied by the phosphorylation of the same residue in the "activation loop" between kinase subdomains VII and VIII (Thr256 in SGK1, Thr193 in SGK2 and Thr253 in SGK3). Moreover, like SGK1 (Example 1 and [18]) and p70 S6 kinase [9], the PDK1-catalysed phosphorylation and activation of SGK2 and SGK3 in

15 vitro is greatly potentiated by mutation to Asp of the C-terminal Ser (Ser422 in SGK1, Ser356 in SGK2 and Ser419 in SGK3), suggesting that phosphorylation of this residue is a prerequisite for the PDK1-catalysed phosphorylation of the activation loop Thr. These observations raise the question of the identity of the protein kinase(s) that phosphorylates SGK

20 isoforms at the C-terminal Ser. PDK1 is converted to a form that phosphorylates PKB at Ser473 as well as Thr308 by interaction with a peptide corresponding to the C-terminal sequence of PRK2 [6]. Whether PDK1 can be converted to a form that phosphorylates SGK isoforms at both sites by interaction with a different protein, or whether this residue is

25 phosphorylated by a distinct protein kinase *in vivo*, remains to be established.

In contrast to SGK1, which is phosphorylated by PDK1 at one major site (Thr256; Example 1 and [18]), SGK2 and SGK3 become phosphorylated at two additional serine residues when incubated with PDK1 and MgATP (Fig 18). SGK2 is phosphorylated at Ser279 and Ser334, as well as

5   Thr193. The sequence surrounding Ser334 (Ser-Ile-Gly-Cys-Thr-Pro-Asp-Thr-Val-Ala) resembles that surrounding Thr193 (Thr-Phe-Cys-Gly-Thr-Pro-Glu-Tyr-Leu-Ala) (Fig 13), suggesting that Ser334 is phosphorylated by PDK1 and raising the possibility that physiological substrates of PDK1 might include proteins that are not kinases. Serines

10   equivalent to Ser334 are present in SGK1 and SGK3 (Fig 3), but are not phosphorylated significantly by PDK1 [18] (Fig 18). The reason for this is unclear, but may be related to the particular amino acid replacements that occur in the vicinity of this residue.

15   Interestingly, Ser279 lies in an Arg-Xaa-Arg-Xaa-Xaa-Ser sequence (Fig 13), which conforms to the optimal consensus for phosphorylation by SGK and PKB [18, 22]. This suggests that Ser279 phosphorylation is likely to be an autophosphorylation event catalysed by SGK2 itself after it has been activated by PDK1. This finding also raises the intriguing possibility that

20   Ser279 may be phosphorylated by another protein kinase *in vivo*, such as another SGK isoform or PKB. It will clearly be of considerable interest to examine whether Ser279 phosphorylation occurs in cells and tissues and whether it alters the catalytic and regulatory properties of SGK2. Ser279 is not conserved in either SGK1 or SGK3 (Fig 13).

25

SGK3 also became phosphorylated at two serines (Ser77 and Ser79) upon incubation with PDK1 and MgATP, which are not conserved in SGK1 or SGK2 (Fig 13). Although these residues do not lie in optimal consensus

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sequences for either SGK or PDK1, they are probably autophosphorylation events catalysed by SGK3 for two reasons. Firstly, activated SGK3 autophosphorylates in the absence of PDK1 (Fig 17F); secondly the SGK3 concentration in these incubations is very high compared to those used with optimal peptide substrates; thirdly, basic residues (Lys74 and His 76) are present three residues N-terminal to Ser 77 and Ser79, which is one of the prerequisites for phosphorylation by SGK.

The response of SGK2 and SGK3 to agonists also differs in several respects from SGK1. For example, SGK2 and SGK3 are activated by IGF1 to a smaller extent (although just as rapidly) as SGK1 (Fig 19). The activation in response to hydrogen peroxide is similar for all three isoforms (five fold), but inhibitors of PI 3-kinase only suppress the activation of SGK2 and SGK3 partially, whereas the activation of SGK1 is abolished (Fig 20). In addition, SGK2 and SGK3 activities are unaffected by exposure to osmotic stress, whereas SGK1 (Fig 19) and PKB [23] activities are virtually abolished. The subcellular localisation of SGK2 and SGK3 may be compared with that of SGK1. These isoforms may translocate to the nucleus or another organelle(s) in response to different agonists in a similar manner to SGK1 [19]. The development of isoform-specific antibodies sufficiently sensitive to detect the endogenous levels of SGK2 and SGK3 may be useful in determining the subcellular location of SGK2 and SGK3.

A number of physiological roles have been ascribed to PKB based on results obtained by overexpression of constitutively active mutants (reviewed in [1, 2]). However, SGK isoforms have a similar specificity to

99

PKB (Table 2) and are activated *in vivo* by the same stimuli. Moreover, SGK1 can mimic the ability of PKB to inactivate glycogen synthase kinase 3 (GSK3) *in vitro* and in cotransfection experiments (Example 1 and [18]). It is therefore possible that some physiological roles thought to be performed by PKB are mediated by an SGK isoform. Conversely, activation of the epithelial sodium channel produced by coexpression with SGK1 in Xenopus oocytes [16] may really mediated by another SGK isoform or by PKB.

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<u>CLAIMS</u>

1.   A method of activating serum and glucocorticoid-induced protein
kinase (SGK) wherein the SGK is phosphorylated.

5

2.   A method of reducing the activity of phosphorylated SGK wherein the
SGK is dephosphorylated.

3.   The method of claim 1 wherein the SGK is phosphorylated by PDK1
10   or a variant, fragment, fusion or derivative thereof, or a fusion of a said
variant, fragment or derivative.

4.   The method of claim 2 wherein the SGK is dephosphorylated by PP1
or PP2C or PP2A or a variant, fragment, fusion or derivative thereof, or a
15   fusion of a said variant, fragment or derivative.

5.   Use of PP1 or PP2C or PP2A or a variant, fragment, fusion or
derivative thereof, or a fusion of a said variant, fragment or derivative in a
method of deactivating and/or dephosphorylating SGK.

20

6.   Use of PDK1 or a variant, fragment, fusion or derivative thereof, or a
fusion of a said variant, fragment or derivative in a method of activating
and/or phosphorylating SGK.

25   7.   A method of activating SGK wherein SGK is phosphorylated on the
residue equivalent to Thr256 of full-length human SGK1.

8.   A method of activating SGK wherein SGK is phosphorylated on the
residue equivalent to Ser422 of full-length human SGK1.

9.   A method according to claim 8 wherein SGK is further phosphorylated on the residue equivalent to Thr256 of full-length human SGK1.

10.   A method according to claim 1 wherein SGK is activated and/or phosphorylated by a preparation containing PDK2 activity.

11.   A fusion polypeptide that comprises human SGK or a variant, fragment or derivative thereof.

12.   A fusion polypeptide according to claim 11 wherein the fusion polypeptide comprises glutathione-S-transferase.

13.   A fusion polypeptide according to claim 11 or 12 or wherein the fusion polypeptide comprises a fragment of human SGK or variant or derivative thereof wherein residues equivalent to the N-terminal about 20, 30, 40, 50 or 60 amino acids of human full-length SGK1 are not present.

14.   A polypeptide comprising the amino acid sequence of human SGK or a fragment, variant, derivative or fusion thereof wherein the residue equivalent to serine 422 of full-length human SGK1 is replaced and/or the residue equivalent to threonine 256 of full-length human SGK1 is replaced and/or the residue equivalent to lysine 127 of full-length human SGK1 is replaced.

15.   A polypeptide according to claim 14 wherein the residue equivalent to serine 422 of full-length human SGK1 is replaced by an aspartate, glutamate, alanine or other non-phosphorylatable residue and/or the

residue equivalent to threonine 256 of full-length human SGK1 is replaced

by an alanine or other non-phosphorylatable residue and/or the residue

equivalent to lysine 127 of full-length human SGK1 is replaced by an

alanine residue.

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16. A polypeptide according to claim 15 wherein the residue equivalent to

serine 422 of full-length human SGK1 is replaced by an aspartate residue

and the residues equivalent to threonine 256 and lysine 127 of the full-

length human SGK1 remain as threonine and lysine respectively.

10

17. A polypeptide according to claim 16 wherein residues equivalent to

the N-terminal 20, 30, 40, 50 or 60 amino acids of full-length human

SGK1 are not present.

15   18. A polynucleotide encoding a polypeptide as defined in any one of

claims 11 to 17 .

19. A recombinant polynucleotide suitable for expressing a polypeptide as

defined in any one of claims 11 to 17.

20

20. A host cell comprising a polynucleotide or as defined in claim 18 or

19.

21. A method of making the polypeptide as defined in any one of claims

25   11 to 17 the method comprising culturing a host cell comprising a

recombinant polynucleotide or a replicable vector which encodes said

polypeptide, and isolating said polypeptide from said host cell.

22. A method according to claim 21 further comprising treating the host cell such that the polypeptide is activated and/or phosphorylated.

23. A method according to claim 22 wherein the host cell is treated by
5   exposing it to IGF-1 and/or hydrogen peroxide.

24. A polypeptide obtainable by the method of any one of claims 21 to 23.

10   25. A method of identifying a compound that modulates the activity of SGK wherein activated SGK is used.

26. A method of identifying a compound that modulates the activity of SGK, the method comprising contacting a compound with SGK and
15   determining whether the activity of the said SGK is changed compared to the activity of the said SGK in the absence of said compound wherein the activity of SGK is measured by measuring the phosphorylation by SGK, in the presence of a suitable phosphate donor, of a polypeptide comprising an amino acid sequence corresponding to the consensus sequence (Arg/Lys;
20   preferably Arg)-X-(X/Arg)-X-X-(Ser/Thr)-Z, wherein X indicates any amino acid, X/Arg indicates any amino acid, with a preference for arginine, and Z indicates that the amino acid residue is preferably a hydrophobic residue.

25   27. The method of claim 25 or claim 26 wherein the said SGK or activated SGK is a SGK wherein the residue equivalent to serine 422 of full-length human SGK1 is replaced by an aspartate residue and the residues equivalent to threonine 256 and lysine 127 of the full-length human SGK1 remain as threonine and lysine respectively.

28. The method of any one of claims 25 to 27 wherein the SGK is SGK activated by phosphorylation.

29. The method of any one of claims 24 to 28 wherein the activity of the SGK is decreased in the presence of the compound.

30. The method according to claim 25 or 26 wherein the activity of the SGK is increased in the presence of the compound.

31. A method of identifying a compound which binds to a physiological substrate of SGK, such as BAD or GSK3, and either enhances or prevents its activation and/or phosphorylation by SGK, the method comprising determining whether a compound enhances or prevents the interaction of the said substrate with SGK or determining whether the compound substantially blocks phosphorylation and/or activation of said substrate by SGK.

32. A method of identifying a compound which modulates the activation of SGK by an interacting polypeptide, such as PDK1 or a polypeptide with PDK2 activity, the method comprising determining whether a compound enhances or disrupts the interaction between (a) SGK and (b) the interacting polypeptide, such as PDK1 or a functional equivalent of PDK1 or a preparation containing PDK2 activity, or determining whether the compound modulates activation of the said SGK by the interacting polypeptide, such as PDK1 or a preparation containing PDK2 activity or a functional equivalent thereof.

106

33. A method of identifying a polypeptide that interacts with activated SGK, the method comprising (1) contacting (a) the said SGK with (b) a composition that may contain a polypeptide that interacts with the said activated SGK, (2) detecting the presence of a complex containing the said

5   SGK and a polypeptide, and optionally (3) identifying any polypeptide bound to the said protein kinase.

34. A kit of parts useful in carrying out a method according to any one of claims 25 to 33.

10

35. A kit of parts according to claim 34 comprising SGK, PDK1 or a functional equivalent thereof, a preparation containing PDK2 activity or a functional equivalent thereof and/or a substrate of SGK, for example Crosstide or BAD or GSK3.

15

36. Use of a compound that inhibits SGK but does not inhibit PKB in a method of identifying a substrate of SGK.

37. A compound identifiable or identified by a method according to any

20   one of claims 25 to 33.

38. A compound according to claim 37 for use in medicine.

39. Use of a compound according to claim 37 in the manufacture of a

25   medicament for treatment of a patient in need of modulation of the activity of SGK.

107

40. A method of treating a patient in need of modulation of the activity of SGK wherein the patient is administered a effective amount of a compound according to claim 37.

5   41. Use of activated SGK in a screening assay for a drug-like compound or lead compound for the development of a drug-like compound.

42. The use according to claim 39 or method according to claim 40 wherein the patient has cancer.

10

43. The use according to claim 39 or method according to claim 40 wherein the patient has diabetes or ischaemic disease.

44. The method, use, fusion polypeptide, polypeptide or kit of parts

15   according to any one of claims 1 to 17, 25 to 33, 35, 39 to 43 wherein the said SGK is SGK1, SGK2α, SGK2β or SGK3.

SGK   TTS**TF**CGTPEYLAPE........FLGF**SY**APP
       256   422

PKBα   TMK**TF**CGTPEYLAPE........FPQF**SY**SAS
       308   473

p70 S6K VTH**TF**CGTIEYMAPE........FLGF**TY**VAP
        229   389

PKCδ   RAS**TF**CGTPDYIAPE........FAGF**SF**VNP
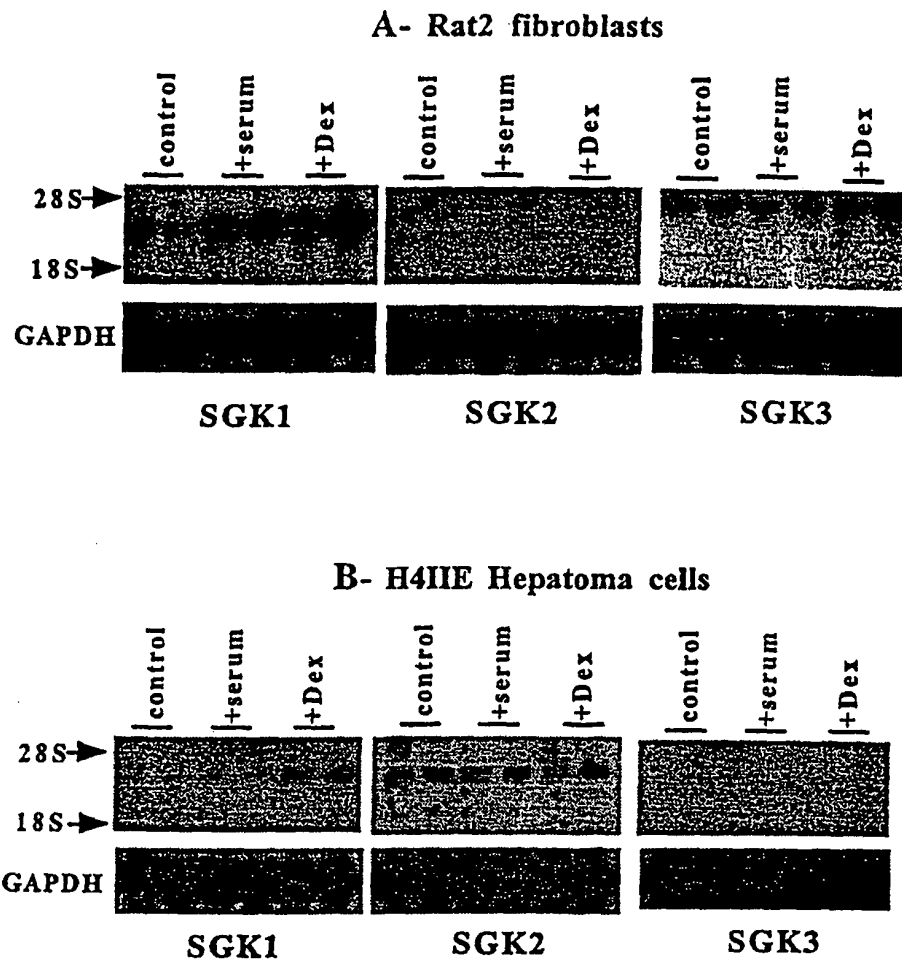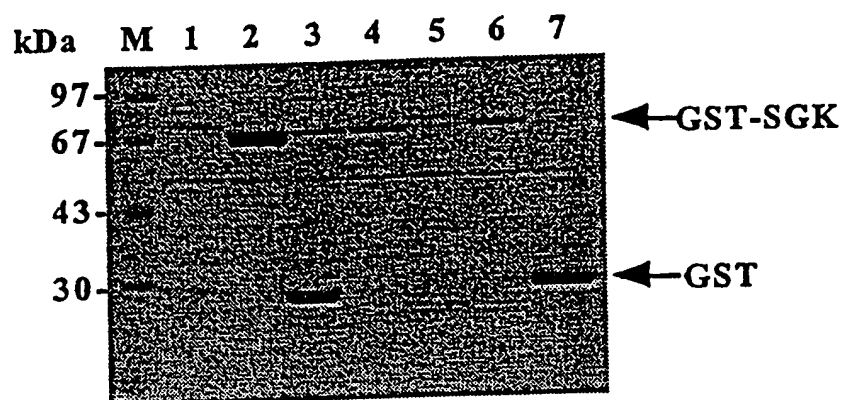   507   664

Figure 1

Fig. 2

Figure 3

A

Fig. 4

B

Fig. 5

Figure 6

Figure 7

Figure 8

Figure 9

Figure 10

A

B

Figure 11

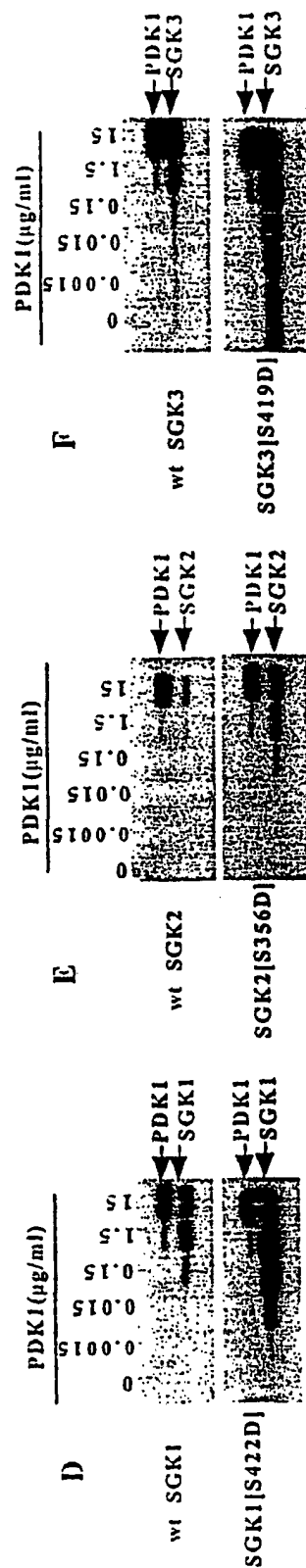Figure 12

Figure 13

Figure 14

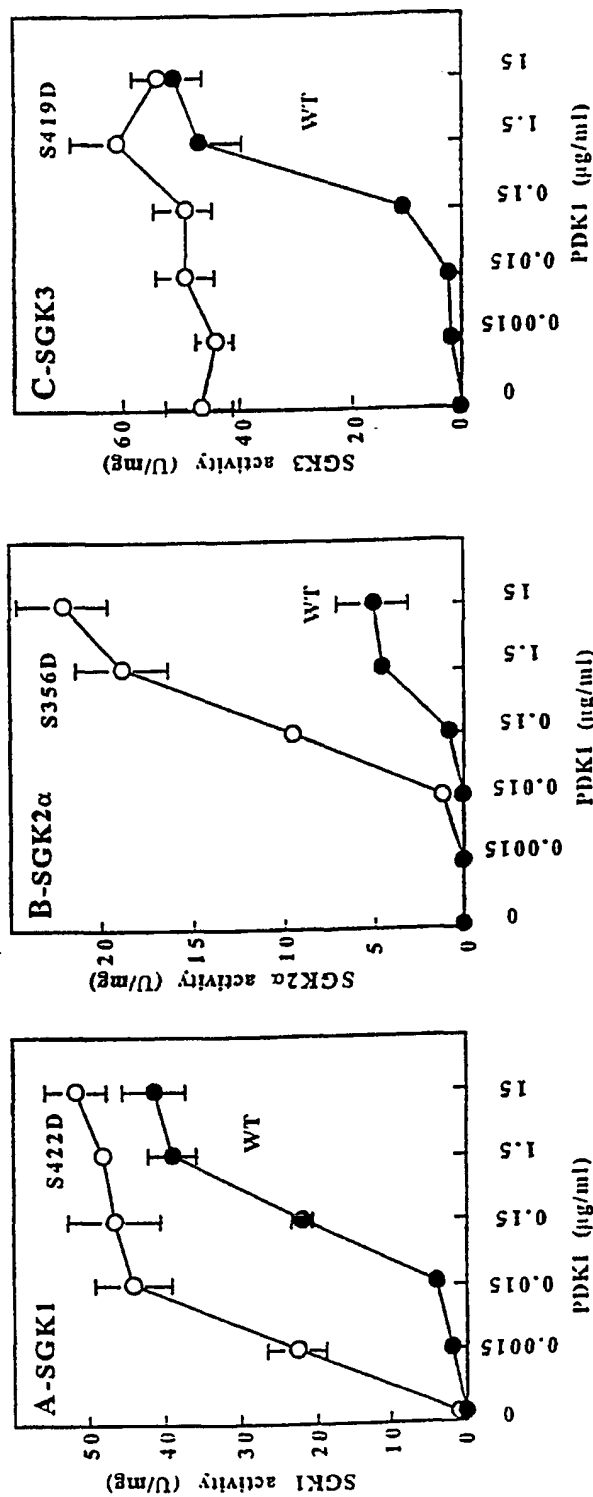A- Rat2 fibroblasts

B- H4IIE Hepatoma cells

Figure 15

Figure 16

Figure 17
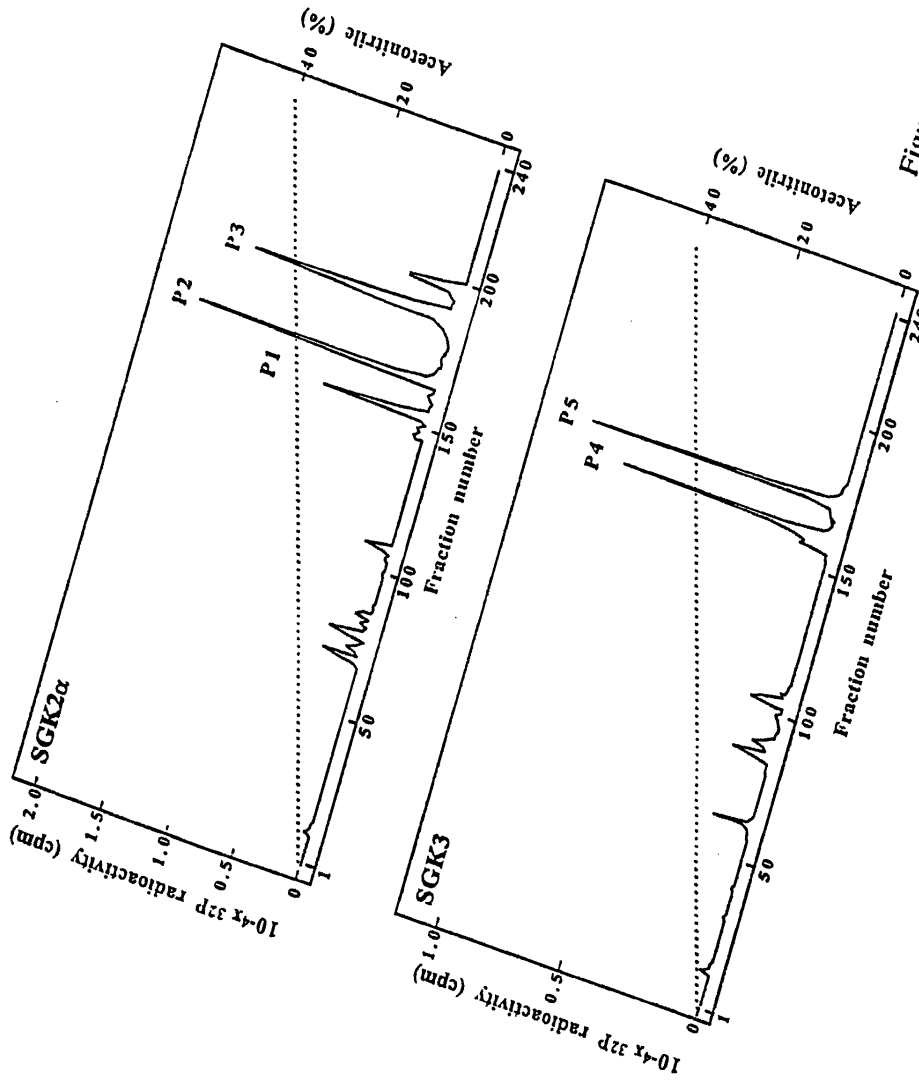
Figure 18
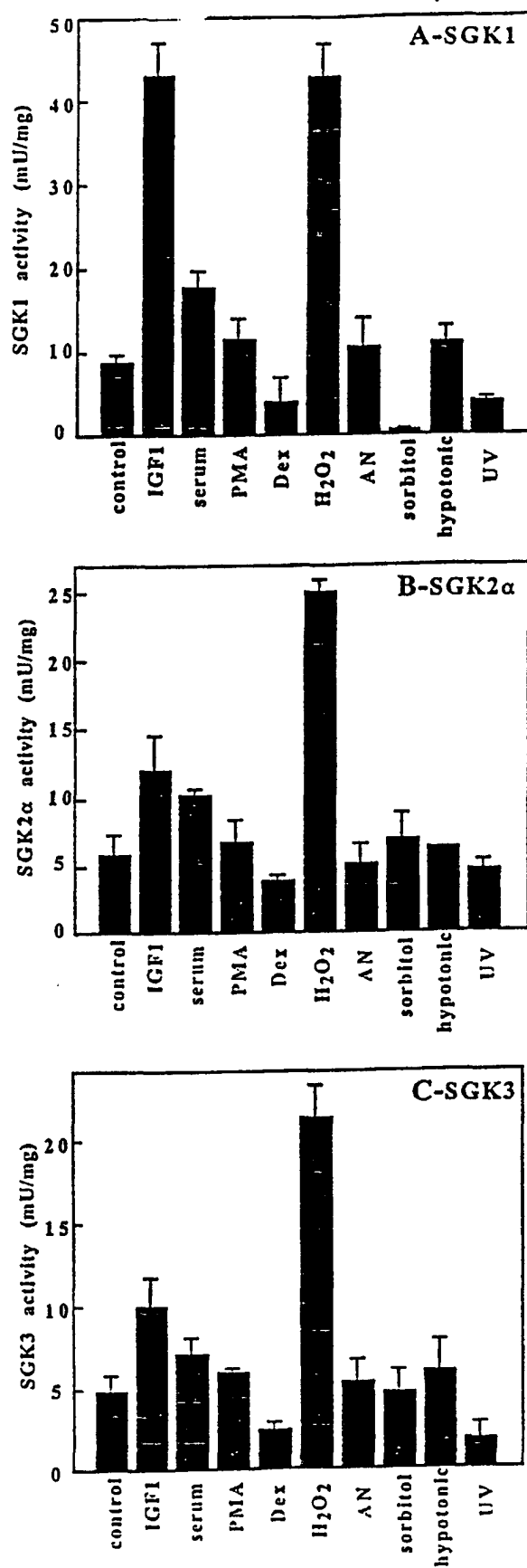
Figure 19
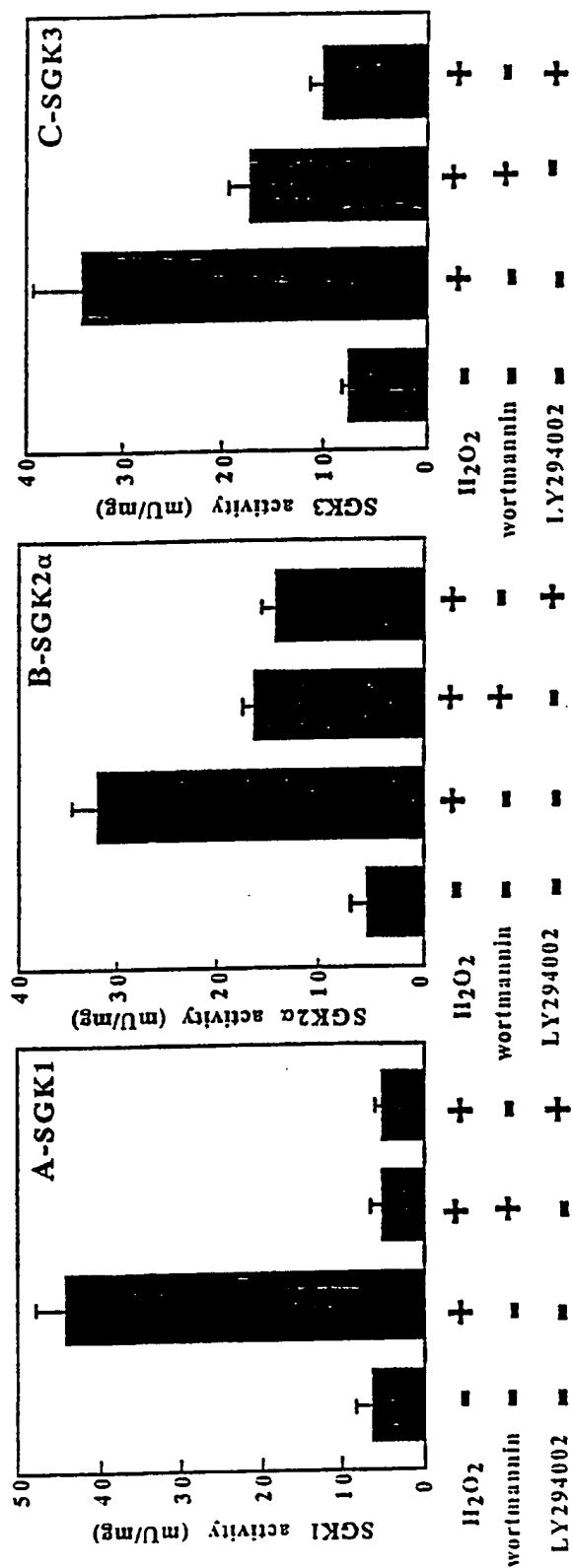
Figure 20

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7   C07K14/435   C12P21/02   C12N9/12   C12N15/54   C12N15/63

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7   C12N   C12P   C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	S. WALDEGGER ET AL.: "Cloning of sgk serine/threonine protein kinase form shark rectal gland- a gene induced by hypertonicity and secretatogues" PFLÜGERS ARCH.-EUR. J. PHYSIOL., vol. 436, 1998, pages 575-580, XP002133634 the whole document ---	1-10,28, 32-35, 40-43
P,X	T. KOBAYASHI ET AL.: "Characterization of the structure and regulation of two novel isoforms of serum- and glucocorticoid-induced protein kinase" BIOCHEM. J., vol. 344, 1999, pages 189-197, XP000881885 the whole document --- -/--	1-10,28, 32-35, 40-43

[X] Further documents are listed in the continuation of box C.   [ ] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 May 2000	3 1. 05. 00

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Marie, A

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	T. KOBAYASHI ET AL.: "Activiation of serum and glucocorticoid regulated protein kinase by agonists that activate phosphatidylinositide 3-kinase is mediated by 3-phosphoinositide dependent protein kinase-1 (PDK1) and PDK2" BIOCHEM. J., vol. 339, 1999, pages 319-328, XP000881886 the whole document -----	1-10,28, 32-35, 40-43

INTERNATIONAL SEARCH REPORT

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
   because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

SEE ADDITIONAL SHEET

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

   1-10,28,32-35,40-43

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

   ☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-10,28,32-35,40-43

   These claims form an inventive concept, as far as they are related to the activation/deactivation of sgk by phosphorylation.

   On the contrary, claims 11-27,29-31,44 have nothing to do with the activation or phosphorylateion of sgk, but are only concerned with sgk itself.They form another inventive concept not directly related to the previous one and hence contravene the provisions of Rule 13 PCT.